

## STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number: 105281

TO: Vanessa L Ford

**Location: CM-1/8A16/8E12** 

Art Unit: 1645

Monday, October 06, 2003

Case Serial Number: 09/771382

From: David Schreiber

**Location: Biotech-Chem Library** 

CM1-6A03

Phone: 308-4292

david.schreiber@uspto.gov

Search Notes	
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	Sy.





From:

Pak, Michael

Sent:

Friday, October 03, 2003 10:39 AM

**T**:

STIC-Biotech/ChemLib

Cc: Subject: Ford, Vanessa RE: ÍN Re: 09771382 Sequence search

Dear STIC,

Please search the multiple sequence search request set forth below. The search is necessary for the examination of the application.

thanks,

#### Mike Pak

-----Original Message-----

Fr m:

Chan, Christina

Sent:

Friday, October 03, 2003 10:24 AM

To:

Ford, Vanessa; Pak, Michael; STIC-Biotech/ChemLib

Subject:

RE: IN Re: 09771382 Sequence search

#### Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644 308-3973 CM-1, 9B19

----Original Message-----

From: Ford, Vanessa

Sent:

Thursday, October 02, 2003 6:46 PM

To: Chan, Christina

Subject: IN Re: 09771382 Sequence search

Please search SEQ ID NOs: 23-27 and 33-39. Please include interference searches. Please rush.

Vanessa L. Ford

Biotechnology Patent Examiner

Office: CM1 8A16 Mailbox: CM1 8E12 Phone: 703.308.4735 Art Unit: 1645

Searcher: Phone: Location: Date Picked Up: Date Completed: Searcher Prep/Review: Clerical: Online time:\_

TYPE OF SEARCH:

NA Sequences: AA Sequences: Structures:

Bibliographic: Litigation: Full text:

Patent Family:\_\_ Other:\_

VENDOR/COST (where applic.)

DIALOG:

Questel/Orbit: DRLink:

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WWW/Internet:\_ Other (specify):\_

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# STIC SEARCH RESULTS FEEDBACK FORM

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Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

Voluntary Results Feedback.FOTH.
> I am an examiner in Workgroup: Example: 1610
> Relevant prior art found, search results used as follows:
☐ 102 rejection
☐ 103 rejection
☐ Cited as being of interest.
Helped examiner better understand the invention.
Helped examiner better understand the state of the art in their technology.
Types of relevant prior art found:
☐ Foreign Patent(s)
<ul> <li>Non-Patent Literature         (journal articles, conference proceedings, new product announcements etc.)</li> </ul>
> Relevant prior art not found:
Results verified the lack of relevant prior art (helped determine patentability).
Results were not useful in determining patentability or understanding the invention.
Comments:

Drop off or sand completed forms to STE/Blotech-Cham Library CM1 – Chc. Dask



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N. meningitidis H4	AAU06172	22	592	Ψ	2207.5	2
surface protei	AAY23744	20	592	ω	207	21
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surface prote	AAY23738	20	598	5	235	9
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                                  25-JAN-2000; 2000US-0177917
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           24-SEP-1999
                               AAY27202;
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                                                   AAY27202
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                                                   standard;
                                                                                                      EAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                EAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                                             MYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEI
                                                                                                                                                                                                                                                                        KEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITV
                                                                                                                                                                                                                                                                                  KEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITV
                                                                                                                                                                                                                                                                                                                 SADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTA
                                                                                                                                                                                                                                                                                                                                                         LNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   512
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         (first
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Pred. No. 7.6
0; Mismatches
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7.6e-142;
es 0;
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Best Local :
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14-JAN-1998;
01-SEP-1998;
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bacterial
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                                                                                                                                                                                                                                                                                                                 458;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Page 62; 123pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid sequence
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 YAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                TNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAG
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meningitidis protein; infection; treatment.
                                                N. meningitidis protein
                pharmaceutical;
                                                   ORF40-1.
                  vaccine;
                   diagnosis;
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98GB-0022143. 98GB-0000760. 98GB-0019015.

New protein and its nucleotide sequence, useful in vaccines diagnostic compositions for treating and/or preventing Neis: Neisseria or

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Rappuoli

₽,

Scarlato

English.

The invention provides proteins (AAY27201-245) from Neisseria meningitidis (Strains A and B) and nucleic acid sequences (AAX99123-167) encoding the proteins. Compositions comprising the protein, nucleic acid or antibody specific to the protein are useful as pharmaceuticals, e.g. a vaccine composition or a diagnostic composition. The composition is also useful for treating or preventing an infection due to Neisserial especially Neisseria meningitidis

99.3%; nilarity 100.0%; Conservative .08; 0; Score 2333; D Pred. No. 1.1 0; Mismatches .1e-140; DB 20; 0; Indels Length 591; 0; Gaps

IAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAG

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423 493

553

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RESULT 3
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                                                                                                                                                                                                                                                                                          The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYQU)
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                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis surface proteins useful for treating meningitidis infections
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                                                                     TKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLYTGKDKGENGSSTDEGEGLYTAKEV 183
                                                                                                                              GATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDEVRTYDTVEFLSAD 123
                                                                                                                                                                                                                                                                                                                                                                                                  Page 104-106; 132pp;
                                                                                                                   GATTNYTNDNYTDDEKKRAASYKDYLNAGWNIKGYKPGTTASDNYDFYRTYDTVEFLSAD
                                                                                                                                                                           TDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNT
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                     TDLTSYGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNT
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                                                                                                                                                                                                                                                            591
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100.0%; Pr
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                                                                                                                                                                                                            Score 2333; DB 20;
Pred. No. 1.1e-140;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                   English.
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                                                                                                                                                                                                                                                                                                                                                                          (ISIS-)
                                                                                                                                                                                                                                                                               Neisseria meningitidis surface proteins useful for treating meningitidis infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-SEP-1999
                                                                                                                  Sequence
                                                                                                                                                                                                                                                         Claim 1; Page 127-128; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Surface protein;
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                                                                                                                                                            prevent or treat N. meningitidis infection in humans,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunoreactive peptide.
                                                                                                                                                   the form of vaccines. The proteins and antibodies can also
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GATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSAD 123
                                  TDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRN
                        TDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNT
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                                                                                                                  591 AA;
                                                                     Conservative
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                                                                               Pred. No. 1.1e-140;
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591;

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                                                                                                                                                                                                                                                                                                                                                                antigen NhhA; meningococcal disease; meningitis vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDV
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                                                                                                                                                                                                                                                                                                                                            meningitidis strain
                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                      /note= "C
230..236
                                                                                                                                                                                                                          /note= "Variable region 52..591
                                                                                                                   /label= V2
/note= "Variable
125..188
                                                                                                                                                                                   109..120
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/note= "Conserved
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                                                                                                                                                                                                                                                                                                                                                                        the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen what from N. meningitidis strain PMC21 is 1 of 10 Nhha polypeptide sequences (AAUG6171-AAUG6180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhhA (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treat preventing broad spectrum of Neisseria meningitidis - \frac{1}{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                   TKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEV
                                                                                                                                                                                                                  GATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSAD
                                                                                                                                                                                                                            GATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSAD
  TNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAG
                                                                                                                                         IDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYD
                                                                                                                                                                       TKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fig 1; 91pp;
                                                                                                                               IDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYD
                                                                                                                                                                                                                                                                                                                                            591
                                                                                                                                                                                                                                                                                                                                                                  invention.
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Pred. No. 1.1e-140;
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Region
                                                                                                                                                   New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis -
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhha (AAUU6182-AAUU6186). The modified or mutant Nhha polypeptides are
                                                                                                      Claim 9;
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DB; AASO9165.
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                                                                                                   Fig 1; 91pp; English.
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YAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= V4
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/note= "Variable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= V2
/note= "Variable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitids, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain EG329 is 1 of 10 NhhA polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                               GATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNT
                     YAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                    TNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAG
                                                                                                                                                                                                                                                                     VNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRN
                                                                                                                                                                                                                                                                                                                               TKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEV
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YAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                TNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAG
                                                                                                                                                                                                                                                VNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRN
                                                                                                                                                                                                                                                                                                                                                                       IDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               591 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.3%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 2333; DB 22;
Pred. No. 1.1e-140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                        461
  591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         591;
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Misc-difference
                                                                                                                     BASB029 amino
         Misc-difference
                                             Misc-difference
                                                                                                    Nisseria meningitidis;
                                                                                                                                                                             standard;
                                                                        meningitidis
                                                                                          treatment;
                                                                                                                                       (first entry)
                                                                                                                      acid
      /note=
                         /note=
92
                                             Location/Qualifiers 90
/note=
                                                                                                                     sequence
                                                                                                                                                                             Protein;
                                                                                          prevent;
"Encoded by AAC"
               "Encoded by
                                    "Encoded
                                                                                                                      from N.
                                                                                                                                                                             591
                                                                                            antibacterial
                                   bу
                                                                                                    surface fibril protein;
                                                                                                                                                                             A
                GAT"
                                    AAT"
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HSF; diagnosis;

H44/76.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serogroup B strain H4/76. The BASB029 protein is homologous to the Haemophilus influenzae surface fibril (HSF) protein. The invention of relates to BASB029 polynucleotide sequences (AAX39864-Z3985) and copypeptide sequences (AAX397044-Y57045) and their immunogenic fragments. BASB029 polypeptides are useful in a method of diagnosing a Neisseria commingitidis infection in a mammal. Compositions containing BASB029 polynucleotides and polypeptides are useful for generating an immune cresponse in an animal. A therapeutic composition comprising an antibody directed against BASB029 is useful in treating humans with Neisseria compitidis disease. The polynucleotide is useful in the diagnosis of the stage of infection, type of infection, susceptibility to an confiction which results from increased or decreased expression of the polynucleotide, and for therapeutic or prophylactic purposes, comparticularly genetic immunisation. Antibodies against BASB029 comparticularly bacterial infections. The protein is useful in the disconstitutions and development of antibacterial drugs. Fused recombinant confictions are also useful in the combinant and confidence and companism of the immune system of an organism confidence and companism of the stimulation of the immune system of an organism confidence and combinant confidence and combinant confidence and combinant combinant combinant combinance and combinant combined the stimulation of the immune system of an organism combined combined combined the stimulation of the immune system of an organism combined co
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptide from neisseria meningitidis useful treatment or prevention of bacterial infections in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruelle
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DB; AAZ39865.
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                                                                                                                                                                                                                                                                 TDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNT
                                                                                                                                                                                                           GATTNYTNDNYTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSAD
VNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRN
                                                                                                                                 TKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEV
                                                                                                                                                                                       GATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSAD
                                                       IDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYD
                                   IDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYD
                                                                                                               TKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                               the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                           591
                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; 74pp; English.
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389
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269
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123
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99.8%;
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                                                                                                                                                                                                                                                                                                                                           Score 2330; DB 21;
Pred. No. 1.7e-140;
1; Mismatches 0;
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BASB029 protein i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        o acid sequence from is homologous to the otein. The invention
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                                                                                                                                                                                                                                                                                                                                                                                 Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                   591;
                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism
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64

GATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSAD

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AAY23737
                                                          Query Match
Best Local S
Matches 457
                                                                                                                                                                                                         The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ISIS-)
                                                                                                                                               The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especial in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Surface protein; immunoreactive po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A surface
                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9931132-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY23737 standard;
                                                                                                                                                                                                                                                                                                                                    meningitidis
                                                                                                                                                                                                                                                                                                                                               Neisseria meningitidis surface
                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                          Jennings MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis
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TDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein of Neisseria meningitidis
                                                                                                                    592
                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                    infections
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                                                                                                                                                                                                                                                                                                                                                                                                                          Moxon
                                                                                                                    ΑĄ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
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                                                                      99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glycoprotein; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                            Peak
                                                     Score 2329; D
Pred. No. 2e-1
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                               proteins useful
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                                                   e 2329; DB 20;
. No. 2e-140;
--+ches 1;
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                                                                                      Length
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                                                          Indels
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n a kit for
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an also
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                                                          Gaps
194
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DB 20;

594; 1;

Indels Length

Gaps

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ID ANY 23740
ID ANY 23740
AC ANY 2
XX AAY 2
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PN W099
PN W099
PN W11-
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The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                            Neisseria meningitidis surface meningitidis infections
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N. meningitidis EG327

surface antigen NhhA polypeptide

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Matches 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASB029 polypeptides are useful in a method of diagnosing a Neisseria meningitidis infection in a mammal. Compositions containing BASB029 polynucleotides and polypeptides are useful for generating an antibody response in an animal. A therapeutic composition comprising an antibody directed against BASB029 is useful in treating humans with Neisseria meningitidis disease. The polynucleotide is useful in the diagnosis of the stage of infection, type of infection, susceptibility to an infection which results from increased or decreased expression of the polynucleotide, and for therapeutic or prophylactic purposes, particularly genetic immunisation. Antibodies against BASB029 particularly genetic immunisation. Antibodies against BASB029 particularly bacterial infections. The polynucleotides and polypeptides are also useful for treating infections particularly bacterial infections. The portein is useful for the stimulation of the immune system of an organism protein is useful for the stimulation of the immune system of an organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haemophilus influenzae surface fibril (HSF) protein. The invention relates to BASB029 polynucleotide sequences (AAZ39864-Z39865) and polypeptide sequences (AAY57044-Y57045) and their immunogenic fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
  24-OCT-2001
                                        AAU06174;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is the Nisseria meningitidis BASB029
group B strain ATCC13090. The BASB029
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97.4%;
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ion of bacterial infections in
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Pred. No. 4.6e-136;
4; Mismatches 7;
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protein is homologous
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the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain EG327 is 1 of 10 NhA polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                      The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen whha (AAU06182-AAU06186). The modified or mutant whha polypeptides are characterised by deletions of non-conserved amino acids, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peak
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                                                                                                                                                                                                                                                                                                                                    preventing broad
                                                                                                                                                                                                                                                                                                                                                           New NhhA surface antigen polypeptides and polynucleotides 
Neisseria meningitidis, useful in producing vaccines for t
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/note= "Variable region
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N-PSDB; AAX85795.
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                                                                                                                                                                                                                                                                                                                                                                                                                     A surface
Claim 1; Page 114-115;
                                 Neisseria meningitidis surface meningitidis infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSKKDNKPVRITNVAPGVKEGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRN
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                                                                                                                                                                                                                                                                                                                                                                                                                   protein of Neisseria meningitidis.
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nilarity 97.4%;
Conservative
                                                                                                                                                            INNOVATION LTD QUEENSLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                              Moxon
                                                                                                                                                                                                                                                                                                                                                                   n; surface peptide.
                                                                                                                                                                                                          97GB-0026398
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                                                                                                                              ER,
 132pp;
                                                                                                                                                                                                                                                                                                                                                                                    glycoprotein; infection;
                                                                                                                              Peak
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Pred. No. 4.6e-136;
4; Mismatches 7;
 English
                                              proteins
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                                                useful
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Best Local :
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                                                                                                                                                                                                                        N. meningitidis
                                                                                                                                                                                                                                                                                                                     AAU06176 standard;
                                                                                                                                                                                                                                                                                     AAU06176;
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              Region
                                                                                                                           Key
                                                                                                                                                          Neisseria
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                                                             Region
                                                                                                            Region
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561 GYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tch 96.1%;
al Similarity 97.4%;
447; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       meningitidis strain
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                                                           /note= '51..105
                                                                                                                                                                                        NhhA;
                106.
                                                                                                                                                                                                                    H38 surface antigen NhhA polypeptide sequence.
                                                                                                                           Location/Qualifiers
                             /note=
                                                                                             /label=
                                              /label=
                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                      entry)
                . 117
                                                                                                                                                                                      meningococcal
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Conserved
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C2
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Pred. No. 7.2e-136;
2; Mismatches 9;
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                             region
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Best Local S
Matches 447
                                                                                                                                                           The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhhA (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain H38 is 1 of 10 NhhA polypeptide sequences (AAU06181) from 10 different N. meningitidis strains given in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                  New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                  25-JAN-2001; 2001WO-AU00069
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                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                      2001-488774/53.
DB; AAS09166.
261
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                                Fig 1;
                 TKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEV
                                                                                                                                      599 AA;
                                                                                                     Conservative
                                                                                                                                                      invention.
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                                                                                                                                                                                                                                                                                   91pp; English.
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/note= "Variable region
244..599
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118..131
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/note= "Conserved
237..243
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132..195
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97.48;
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Pred. No. 7.26
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RESULT 14
AAY23739
Query Match
Best Local Similarity
Matches 446; Conserv
                                                                                                          The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionall a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humanghem. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especiall in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis surface proteins useful meningitidis infections
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                                                                           Sequence
                                                                                                                                                                                                                                                                                                    Claim 1;
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DB; AAX85791.
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213..23
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127..19
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117..1
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                           GATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSAD
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meningitidis mutant polypeptides of the surface antigen NhhA (AAU06182-AAU06186): The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain BZ198 is 1 of 10 NhhA polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New NhhA surface antigen polypeptides and polynucleotides Neisseria meningitidis, useful in producing vaccines for t preventing broad spectrum of Neisseria meningitidis -
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

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; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-11
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US-09-377-155-11
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PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-2-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 591
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CURRENT FILING DATE: 1999-08-19
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458; Conserv
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                                                                  VNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRN
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US-09-377-155-32
US-09-69-974-32
US-09-68-347-4
US-08-913-942-2
US-09-68-467-5
US-08-913-942-5
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US-08-913-942-15
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FILE REFERENCE: 065064/0128
FILE REFERENCE: 055064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
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; TYPE: PRT
; ORGANISM: Neisseria meningitidis
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Matches 458
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APPLICANT: PEAK, Ian Richard
APPLICANT: JENNINGS, Michael
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SUF
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LENGTH: 591
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SOFTWARE: PatentIn V
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GKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDV
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RESULT

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Sequence 21, Application US/09669974
Patent No. 6333173
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANT
FILE REFERENCE: 065064/0128

CURRENT APPLICATION

NUMBER: US/09/669,974

SURFACE ANTIGEN

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CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEO ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
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LENGTH: 591
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APPLICANT: JENNINGS, Michard
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURF
FILE REFERENCE: 065064/0128
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Sequence 2, Application US/09377155
Patent No. 6197312
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTI
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PRIOR APPLICATION NUMBER: US 09/377,155;
PRIOR APPLICATION NUMBER: PCT/AU98/01031;
PRIOR APPLICATION NUMBER: PCT/AU98/01031;
PRIOR FILING DATE: 1998-12-14;
PRIOR FILING DATE: 1997-12-12;
PRIOR FILING DATE: 1997-12-12;
PRIOR FILING DATE: 1997-12-12;
NUMBER OF SEQ ID NOS: 33;
SOFTWARE: Patentin Ver. 2.0;
SEQ ID NO 21;
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; ORGANISM: Neisseria meningitidis
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                                                     PRIOR APPLICATION NUMBER: PCT.
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9
PRIOR FILING DATE: 1997-12-12
                                                                                                                     CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
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                              Ver.
                                                                                                                                                                 NOVEL SURFACE ANTIGEN
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ER: US 09/377,155
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                                                                          GB 9726398.2
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US-09-669-974-2
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APPLICANT: PEAK, IA
APPLICANT: JENNING
                                                     Matches
                                                               Query Match
Best Local
                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2,
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PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997 12-12
                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NOVEL SURFACE ANTIGEN FILE REFERENCE: 065064/0128
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APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 33
                                                                                                                                 LENGTH: 592
TYPE: PRT
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                                                                Similarity
            TDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNT
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TDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNT 194
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                                                                Score 2329; DB 4;
Pred. No. 3.1e-180;
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT FILLING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-12-14
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: B9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 594
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; TYPE: PRT
; ORGANISM: Neisseria
US-09-377-155-9
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US-09-377-155-9
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YAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
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97.4%;
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; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria m
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CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
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Matches 447
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APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE A
FILE REFERENCE: 065064/0128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 33 SOFTWARE: Patentin Ver. :
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447; Conserv
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                              GKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSKKDNKPVRITNVAPGVKEGD
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Pred. No. 1.1e-174;
4; Mismatches 7;
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RESULT 10
US-09-669-974-15
; Sequence 15, Application
; Patent No. 6333173
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, LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-15
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CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
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Patent No. 6197312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: PEAK, Ian Richard Anselm APPLICANT: JENNINGS, Michael Paul APPLICANT: MOXON, E. Richard TITLE OF INVENTION: NOVEL SURFACE AN ETLE REFERENCE: 06564/0128
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APPLICANT:
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cal Similarity 97.4%;
447; Conservation
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                  US/09669974
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Pred. No. 1.9e-174;
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Sequence 7, Application US/09377155;
Patent No. 6197312;
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128;
CURRENT APPLICATION NUMBER: US/09/377,155;
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031;
PRIOR FILING DATE: 1998-12-14
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APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 1999-08-19
PRIOR PILING DATE: 1999-08-19
PRIOR PILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
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; ORGANISM: Neisseria meningitidis
US-09-669-974-15
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US-09-377-155-7
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Best Local Similarity
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                                                                      NOVEL SURFACE ANTIGEN
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Gaps

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APPLICANT: JENNINGS, MICHAEL PAUL
APPLICANT: MOXON, E. RICHAEL
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-12-14
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
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; ORGANISM: Neisseria meningitidis US-09-669-974-7
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US-09-669-974-7
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Best Local S
Matches 446
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PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 594
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APPLICANT: PEAK, Ian Richard Anselm
                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application Patent No. 6333173
                                                                SEQ ID NO
                                   TYPE: PRT
                                                 LENGTH:
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46; Conservative
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97.2%;
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US-09-377-155-5
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE A
                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Vo
SEQ ID NO 5
LENGTH: 598
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Best Local S
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CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR EILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
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                                                       TDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGDPTVHLNGIGSTLTDTLLNT
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Pred. No. 1.2e
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APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michard
APPLICANT: JENNINGS, Michard
TITLE OF INVENTION: NOVEL SUFFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 199-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                            GATTNYTNDNYTDDEKKRAASYKDYLNAGWNIKGYKPGTTASDNYDFYRTYDTYEFLSAD
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APPLICANT: PEAK, Ian Richael Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: DS 9726398.2
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
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PRIOR FILING DATE: 1997-12-12
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Pred. No. 1.2
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Search completed: October 6, 2003, 09:35:56
Job time: 13.3281 secs

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Minimum
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Perfect score:
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length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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    /cgn2_6/ptodata/2/pubpaa/US09C_MEW_PUB.pep:*
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US-09-797-862-11

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US-09-771-382-3

US-09-771-382-3

US-09-797-862-9

US-09-797-862-15

US-09-771-382-6

US-09-771-382-6

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ALIGNMENTS	US-09-797-862-13 US-09-771-382-7 US-09-771-382-36 US-09-771-382-36 US-09-771-382-34 US-09-771-382-34 US-09-771-382-27 US-09-771-382-10 US-09-771-382-11 US-09-771-382-11 US-09-771-382-38 US-09-771-382-38 US-09-771-382-38 US-09-771-382-38 US-09-771-382-39 US-10-175-282-3 US-10-175-282-3 US-10-175-282-3 US-10-193-764-61 US-10-193-764-61 US-10-193-764-59
	Sequence 13, Applisequence 7, Applisequence 34, Applisequence 34, Applisequence 27, Applisequence 27, Applisequence 27, Applisequence 27, Applisequence 31, Applisequence 31, Applisequence 31, Applisequence 26, Applisequence 27, Applisequence 28, Applisequence 37,

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US-09-771-382-35
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Patent No. US20020160016A1
GENERAL INFORMATION:
APPLICANT: Peak, Ian
APPLICANT: Jennings, Michael
TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
FILE REFERENCE: 8795-24U1
                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 35
                                                                                                                                                                                                                                                                 Matches 461;
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/771,382 CURRENT FILING DATE: 2001-01-25 PRIOR APPLICATION NUMBER: US 60/177,917 PRIOR FILING DATE: 2000-01-25 NUMBER OF SEQ ID NOS: 52 SOFTWARE: Patentin version:3.0
                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 461
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181 KEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITV 240
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                                                                                                                                61 LNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDEVRTYDTVEFL 120
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                                       SADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTA
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                                                                                                                                                                                                                                                             100.0%; So 100.0%; P. ative 0;
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Pred. No. 3.7e-175;
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RESULT 2
US-09-771-382-23
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Best Local S
Matches 461
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APPLICANT: Peak, Ian
APPLICANT: Jennings, Michael
TITLE OF INVENTION: MODIFIED
FILE REFERENCE: 8795-2401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23, Application U Patent No. US20020160016A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/177,917
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
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CURRENT FILING DATE: 2001-01-25
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TYPE: PRT
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ENGTH: 512
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                              GDYTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRG
                                                                MYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEI
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                GDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRG
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Pred. No. 4.2e-175;
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US-09-797-862-11
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CURRENT FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: PCT/MU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Vér. 2.1
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Best Local S
Matches 458
Sequence 21, Application U
Patent No. US30020102276A1
GENERAL INFORMATION:
APPLICANT: PEAK, IAN RICH
APPLICANT: JENNINGS, MIC
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LENGTH: 591
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EAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
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               IAN RICHARD ANSELM
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APPLICANT: Peak, Ian
APPLICANT: Jennings, Michael
APPLICANT: Jennings, Michael
TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
FILE REFERENCE: 8795-2401
CURRENT APPLICATION NUMBER: US/09/771,382
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 60/177,917
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 52
NUMBER OF SEQ ID NOS: 52
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LENGTH: 591
TYPE: PRT
ORGANISM: Neisseria meningitidis
US-09-797-862-21
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CURRENT FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
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                                               SOFTWARE: PatentIn version EQ ID NO 1
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TITLE OF I
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LENGTH: 591
TYPE: PRT
ORGANISM: Neisseria
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|YAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
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; SOFTWARE: PatentIn version 3.0; SEQ ID NO 5; LENGTH: 591; TYPE: PRT; ORGANISM: Neisseria meningitidis US-09-771-382-5
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US-09-771-382-5
; Sequence 5, Application US/09771382
; Patent No. US20020160016A1
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APPLICANT: Peak, In
APPLICANT: Jennings, Michael
TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
FILE REFERENCE: 8795-2401
                                                                                                                                                   Matches
                                                                                                                                                                               Query Match
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Best Local
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CURRENT FILING DATE: 2001-01-25
                                                                                                                                                                 Local Similarity
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; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-797-862-2
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US-09-797-862-2
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APPLICANT: JENNINGS, MICHAEL PAUL
APPLICANT: MOXON, E. RICHARD
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0134
CURRENT APPLICATION NUMBER: US/09/797,862
CURRENT FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR PILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
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Best Local S
Matches 457
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LENGTH: 592
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         GKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDV
                                                    VNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRN
                                                                                          IDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYD
                                                                                                                                                      TKTTTVNVESKDNGKKTEVKIGVKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEV
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                                     VNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRN
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RESULT 9
US-09-797-862-9
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US-09-771-382-33
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US-09-771-382-33
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Best Local Sim
Matches 457;
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TITLE OF INVENTION: MODIFIED SURFACE ANTI-
FILE REFERENCE: 8795-2441
CURRENT APPLICATION NUMBER: US/09/771,382
CURRENT FILING DATE: 2001-01-25
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       Application US/09797862
                                                                              YAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
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Pred. No. 2.
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423 442

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142 63

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GENERAL INFORMATION:
APPLICANT: Peak, Ian
APPLICANT: Jennings, Michael
APPLICANT: Jennings, Michael
TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
FILE REFERENCE: 8795-24U1
CURRENT APPLICATION NUMBER: US/09/771,382
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 60/177,917
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 52
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APPLICANT: MOXON, E. RICHAED
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 055064/0134
CURRENT APPLICATION NUMBER: US/09/797,862
CURRENT FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
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Best Local
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556 TKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKDKGENDSSTDKGEGLVTAKEV 315
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PatentIn version
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APPLICANT: PEAK, IAN RICHARD ANSELM
APPLICANT: JENNINGS, MICHARD PAUL
APPLICANT: MOXON, E. RICHARD
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0134
CURRENT FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: US/09/797,862
CURRENT FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEO ID NOS: 33
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                                                   ; TYPE: PRT ; ORGANISM: Neisseria US-09-797-862-15
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US-09-797-862-15
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SEQ ID NO 15
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Patent No. US20020102276A1
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             96.1%;
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97.4%;
; Score 2257.5; Pred. No. 8.6e 2; Mismatches
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es 9;
                          DB 10;
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TDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNT

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Sequence 6, Application US/09771382
Patent No. US20020160016A1
GENERAL INFORMATION:
APPLICANT: Peak, Ian
APPLICANT: Jennings, Michael
TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
FILE REFERENCE: 8795-2401
CURRENT APPLICATION NUMBER: US/09/771,382
CURRENT FILING DATE: 2001-01-25
CURRENT FILING DATE: 2001-01-25
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PRIOR FILING DATE: 2001-01-25
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
LENGTH: 599
Type: ~~~
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US-09-771-382-6
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US-09-771-382-6
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CURRENT FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 7
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; TYPE: PRT
; ORGANISM: Neisseria
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Matches 446
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APPLICANT: MOXON, E. RICHARD
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
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                                                                      GATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSAD
                      GKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSKKDNKPVRITNVAPGVKEGD
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 GYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
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Pred. No. 4.3e
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No. 4.3e-167;
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; Sequence 5, Application US/09797862; Patent No. US20020102276A1; GENERAL INFORMATION:
; APPLICANT: PEAK, IAN RICHARD ANSELM APPLICANT: JENNINGS, MICHARL PAUL APPLICANT: MOXON, E. RICHARD ANTITLE OF INVENTION: NOVEL SURFACE ANTITLE REFERENCE: 065064/0134
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US-09-771-382-9
; Sequence 9, Application US/09771382
; Patent No. US20020160016A1
; GENERAL INFORMATION:
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LENGTH: 594
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CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 60/177,917
PRIOR FILING DATE: 2000-01-25
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APPLICANT: Jennings, Michael
TITLE OF INVENTION: MODIFIED:
FILE REFERENCE: 8795-24U1
CURRENT APPLICATION NUMBER: US/09/797,862
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TYPE: PRT
ORGANISM: Neisseria
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Similarity 97.2%;
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Pred. No. 4.3e-167;
1; Mismatches 11;
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; TYPE: PRT
; ORGANISM: Neisseria
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Best Local Similarity 96.3%;
Matches 442; Conservative
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SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 5
LENGTH: 598
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PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
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                                              VTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEA
                                                                                          GKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSKKDNKPVRITNVAPGVKEGD
VNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRN
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Pred. No. 4.5e-166;
3; Mismatches 13; 1
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Search completed: October 6, 2003, 10:19:47 Job time: 24.0934 secs

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3: sp_fungi:*
4: sp_human:*
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6: sp_mammal:*
7: sp_mhc:*
8: sp_organel1:
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
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	Q8XDG4	16	1588	15.5	365	8
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Q9f3x6 pasteurella	Q9F3X6	16	1299	17.2	405	ű
Q8gm77 haemophilus	Q8GM77	ນ	1004	23.9	561	4
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Q8gm79 haemophilus	Q8GM79	N	1096		868.5	9
	Q48152	N	1098		874	8
P71401 haemophilus	P71401	N	2353		901.5	27
Q93qy1 neisseria m	Q93QY1	N	589		2069.5	6
Q9jps5 neisseria m	Q9JPS5	N	600		2075.5	5
Q9jpiO neisseria m	Q9JPIO	N	589		2081.5	4
Q9jqw4 neisseria m	Q9JQW4	16	592		2089.5	ω
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	Q9JPR7	N	598		117	1
Q9jps8 neisseria m	Q9JPS8	ນ	. 599		123	õ
Q93qy2 neisseria m	Q93QY2	N	592	93.9	207	9
Q9jpt0 neisseria m	Q9JPT0	N	598	95.1	2235.5	8
Q93qy5 neisseria m	Q93QY5	N	598	95.1	235	7

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EMBL; AF157606; AAK68867.1; -
InterPro; IPR005594; YadA.
Pfam; PF03895; YadA; 1.
SEQUENCE 591 AA; 62048 MW; CODC600798859C6
                                                                                                                                                                                                                                                Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M. "Identification and characterization of a gene encoding a now membrane protein of Neisseria meningitidis.";
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                                                                                                                                                                                                                                                                                      STRAIN=EG329;
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.
RA Moxon E.R., Grandi G., Rappuoli R.;
"Identification of Vaccine Candidates Against Serogroup B
"Interpro; Ilaid-1820(2000).
RE EMBL, AF286365; AAF42515.1; -.
R Fram; PF03895; YadA; 1.
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01-OCT-2000
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Bacteria; Proteobacteria;
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Pred. No. 7.2e-94;
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SPECIES-N.meningitidis; STRAIN-PMC21;
SPECIES-N.meningitidis; Dieckelman M., Moxon R
Peak I.R., Srikhanta Y., Dieckelman M., Moxon R
"Identification and characterization of a gene membrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ de
EMBL; AF226375; AAF42524.1; -.
EMBL; AF226367; AAF41395.1; -.
EMBL; AF226367; AAF42516.1; -.
                                                                                                                                                                                                                     "Complete MC58.";
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Neisseria meningitidis, and
Neisseria meningitidis (serogroup B).

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
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MEDLINE=20175755; PubMec
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STRAIN=MC58 / Serogroup B, BZ169,
MEDLINE=20175756; PubMed=10710308;
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                       Peak I.R., Srikhanta Y., Dieckelman M., Moxon E "Identification and characterisation of a gene membrane protein of Neisseria meningitidis."; Submitted (FEB-199) to the EMBL/GenBank/DDBJ EMBL; AF125375; AAK09243.1; -. IPR005594; YadA. Pfam; PF03895; YadA; 1. SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5
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EMBL, AF226377; AAF42526.1; -.
InterPro; IPR005594; YadA.
Pfam: PF03895; YadA; 1.
                                                                                                                                                                                     MEDLINE-20175756; PubMed=10710308; Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' Comanducci M., Jennings G.T., Baldi L., Bartolini E., Cape Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M. Ratti G., Santini L., Savino S., Scarselli M., Storni E., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettel Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Ven Moxon E.R., Grandi G., Rappuoli R.;
"Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=NG6/88; MEDLINE=20175756;
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Bacteria; Proteobacteria;
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"Identification of Vaccine Candidates Against Serogroup B
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Outer membrane protein G
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Science 287:1816-1820(2000).
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MEDIJINE-20175756; PubMed=10710308;
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti ?
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
MOXON E.R., Grandi G., Rappuoli R.;
"Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
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01-OCT-2000
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Bacteria; Proteobacteri
Neisseriaceae; Neisseri
                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                       Meningococcus by Whole-Genome
Science 287:1816-1820(2000).
EMBL; AF226371; AAF42520.1; -.
InterPro; IPR005594; Yada.
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. 15, Last sequence up
. 22, Last annotation
GNA992.
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O1-OCT-2000 (TrEMBLrel.
O1-OCT-2000 (TrEMBLrel.
O1-OCT-2002 (TrEMBLrel.
Outer membrane protein GNA992.
Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                             MEDLINE-20175756; PubMed-10710308;
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
Moxon E.R., Grandi G., Rappuoli R.,
"Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
EMBL; AE226378; AAR42527.;
TTENDARGEO. V=7.1
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Neisseriaceae; Neisseria.
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NCBI_TaxID=487
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 IDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYD
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98.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Betaproteobacteria;
                                                                                                                                                                                                                                        Score 2281.5; DB 2;
Pred. No. 1.2e-91;
2; Mismatches 5;
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Q93QY4;
01-DEC-2001
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01-OCT-2002 (TrEMBLrel.
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Bacteria; Proteobacteria;
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VTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEA
                                  GKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPVRITNVAPGVKEGD
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REQUENCE FROM N.A.

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RC STRAIN=NG3/88, and BZ232;

RX MEDLINE=20175756; PubMed=10710308;

RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,

RA Comanducci M., Jennings G.T., Baldi L., Marchetti E., Mora M., Nuti S.

RA RACTI G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

RA RACTI G., Santini E., Knapp B., Blair E., Mason T., Tettelin H.,

RA HOOD D. W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

RA MOXON E.R., Grandi G., Rappuoli R.;

"Identification of Vaccine Candidates Against Serogroup B

Meningococcus by Whole-Genome Sequencing.";

RI Science 287:1816-1820(2000).

DR EMBL; AF226376; AAF42525.1; -.

DR EMBL; AF226369; AAF42518.1; -.

DR EMBL; AF226369; AAF42518.1; -.

DR EMBL; AF226399; YadA, 1.

"fam: PF03895; YadA, 1.

"Aa: 62086 MW; 1B25E03B90D04B46 CRC64;
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"Identification of Vaccine Candidates Against Serogroup B
                                                                                                                                                                                                                                                                                                                                                                                                                                  Meningococcus by Whole-Genome (
Science 287:1816-1820(2000).
Science 287:1816-1820(2000).
EMBL; AF2256379; AAAF42528.1; -.
InterPro; IPB005594; YadA.
Pfam; PF03895; YadA; 1.
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NCBI_TaxID=487;
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MEDLINE=20175756; PubMed=10710308;
MEDLINE=20175756; PubMed=10710308;
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                                               VTNVAQLKGVAQNLNNHIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEA
                                                                                            GKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPVRITNVAPGVKEGD
                                                                                                                                          VNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRN
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315 243 375 303 303 435 495

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C. STRAIN-NGH38;

(X. MEDLINE-20175756; PubMed=10710308;

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(A. Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

(A. Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,

(A. Comanducci M., Jennings G.T., Baldi L., Barchetti E., Mora M., Nuti S.,

(A. Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

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(A. Ratti G., Santini L., Knapp B., Blair E., Mason T., Tettelin H.,

(A. Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

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Q9JPR8;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
Q1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Q1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Q1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Q1-Q12 (TrEMBLrel. 22, Last annotation update)
Q12 (TrEMBLrel. 22, Last annotation update)
Q13 (Q14 (Q15) 
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2; Mismatches 9;
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Q9JPH7;
01-OCT-2000
01-OCT-2000
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Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.

Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti

Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

HOOD D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

Moxon E.R., Grandi G., Rappuoli R.;

"Identification of Vaccine Candidates Against Serogroup B

Meningococcus by Whole-Genome Sequencing.";

Science 287:1816-1820(2000).
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SEQUENCE
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NCBI_TaxID=487;
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Bacteria; Proteobacteria;
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"Identification of Vaccine Candidates Against Serogroup B. Meningococcus by Whole-Genome Sequencing.";
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"Identification of Vaccine Candidates Against Serogroup B
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AG43_ECOLI STANDARD,
P39180; P75614; P76360; P97241; Q46771;
P39180; P75614; P76360; P97241; Q46771;
P39180; P75614; P76360; P97241; Q46771;
P39180; P97241; P97241;
P39180; P97241; P97241; P97241;
P39180; P97241; P97241; P97241;
P39180; P97241; P97241; P97241; P97241;
P39180; P97241; P972
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EMBL; AE000237; AAC74487
EMBL; D90778; BAA1809.1
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EMBL; D90779; BAA1881.1
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ECOGene; EG11307; ydba.
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                                                                                        Escherichia coli.
Bacteria; Proteobacteria;
SEQUENCE FROM N.A.
                                                                   Enterobacteriaceae;
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                                           NCBI_TaxID=562;
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B83A12C8B53220EE
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protein).
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SEQUENCE FROM N.A.
STRAIN-ML 308-225;
Henderson I.R., Owen I
Submitted (JAN-1997)
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                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sentities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science
[2]
         EMBL;
EMBL;
EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                            Henderson I.R., Meehan M., Owen P.;
"Antigen 43, a phase-variable bipartite outer membrane protein, determines colony morphology and autoaggregation in Escherichia K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
"A 460-kb DA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map.";
DNA Res. 3:379-392(1996).
                                                                                                                                                                                                                                                                                                 FEMS
                                                                                                                                                                                                                                                                                                                                                                                                        "Comparing the predicted and observed properties in the genome of Escherichia coli K-12."; Electrophoresis 18:1259-1313(1997).
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MEDLINE=97443975; PubMed=9298646;
Link A.J., Robison K., Church G.M.
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MEDLINE=89291704; P
Caffrey P., Owen P.
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                                                               EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43, a unique protein 
Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Purification and N-terminal sequence of the 43, a unique protein complex associated with
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MEDLINE=97426617; PubMed=9278503;
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                                                                                                                                                                                                   SUBCELLULAR SIMILARITY:
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                                                                                                                                                                                                                                            CHAIN) ANCHORED
                                                                                                                                                                                                                                                                                    FUNCTION:
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FUNCTION: CONTROLS COLONY FORM VARIATION
                      D90838;
D90839;
U24429;
                                                               AE000291; AAC75061.1; ALT_INIT.
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BAA15832.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF03797; Autotransporter; 1. Pfam; PF03212; Pertactin; 1.
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nes 112; Conserv
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                                                                                                                                                             NVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMA
                                                                                                                                                                                                                                                                                                                                     DQG-NITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNI
                                                                                                                                                                                                                                                                                                                                                                                                                         DAVNKAGWRM-----KTTTANGQTGQADKFETVTSGTNVTFASG----KGTTATVSKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTVINDKGWQV--VKPGTVATDTV--VNTGAEGGPDAENGDTGQFVRGDAVRTTIN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETAGTNGDTTVHLNGI-----GSTLTDTLLNTGATTNV----TNDNVTDDEK----KRAAS
                                            VNGGLFTARGGTLAGTTTLNNGAILTLSGKTVNN
                                                                                    IGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGN
                                                                                                                                                                                                             DDGGTLDV-RNG-----GTATT-----VSMGNGG----VLLADSGAAVSGTRSDGK-----
                                                                                                                                                                                                                                                        NAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVRIT
                                                                                                                                                                                                                                                                                                  --GINRLGAFSVVEGKADNV-VLENGG-RLD---
                                                                                                                                                                                                                                                                                                                                                                                 -- VNSDGWQIVKNGGVAGNTTVN-QKGRL-QVDAGGTATNVTLKQGGALVTSTAATVT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -KNGRQIVRAEGTANTTVV-----YAGGDQTVHGHALDTTLNGGYQYVHNGGTASDTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VKDVLN-AGWNIKGVKPGTTASDNVDFVRT-----YDTVEFLSADTKTTTVNVES
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IPR004899; Pertactin.
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24.78;
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QGT -> I S -> I C Q -> I S -> 
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Pred. No. 0.02:
63; Mismatches
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SL -> N
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ID OMPA_APR
AC 01-APR
AC 01-APR
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                                                                                                                                                                   Query Match
Best Local S
Matches 138
                                                                                                                                                                                                                                                        REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE-90354033; PubMed-2117568;
Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;
"A protective protein antigen of Rickettsia rickettsii has repeated, near-identical sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 14, Last sequence update)
Outer membrane protein A precursor (190 kDa antigen) (Cell surface antigen) (rOmp A).
OMPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OMPA_RICRI STANDARD; PRT; 22
P15921;
Ol-APR-1990 (Rel. 14, Created)
Ol-APR-1990 (Rel. 14, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
REPEAT
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entitles requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A protective protein annual repeated, near-identical sequences."; Infect. Immun. 58:2760-2769(1990).
-i- FUNCTION: ELICITS PROTECTIVE IMMUNITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Alpl
Rickettsiaceae; Rickettsieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF03797;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR006315; Autotransport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: CELL WALL. S-LAYER WITH HEXAGONAL SYMMETRY.
832
                                                                                 776
                                                                                                                                                                   al Similarity
138; Conserv
                                       51
                                                                                                                         ᆫ
NAASVLTLTNANAVLTGAVDNTTGGDNVGVLNLNGALSQVTGDIGNTNSLATISVGAGTA 891
                                     GIGSTLTDTLLN---TGATTNVT-NDNV---
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                                                                                    DNTTGGDNVGVLNL - - -
                                                                                                                         NNETDLTSVGTEKLSFSANGNKVNITSD---TKGLNFAKETAGTN-----GDTTVHLN
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1180
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24.48;
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                                                                                 -NGALSQVTGDIGNTNSLATISVGAGTATLGGAVIKATTTKLT
                                                                                                                                                                   45;
                                                                                                                                                                                                                                                        W.
                                                                                                                                                                                       Score 179.5;
Pred. No. 0.
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                                                                                                                                                                      Mismatches
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A9D6646C089DF087 CRC64;
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Glycoprotein.

TANDEM REPEATS

Length Indels

2249; 181;

Gaps

831 50

74

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                                                                                                                                                                                                                                       Uphoff T.S., Welch R.A.;
"Nucleotide sequencing of the Proteus mirabilis calcium-independent hemolysin genes (hpmA and hpmB) reveals sequence similarity with the Serratia marcescens hemolysin genes (shiA and shiB).";
J. Bacteriol. 172:1206-1216(1990).
-I- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
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                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE STRAIN-ISOlate 477-12;
MEDLINE-90170827; PubMed-2407716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
Enterobacteriaceae; Proteo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1990 (Rel. 15,
01-AUG-1990 (Rel. 15,
01-NOV-1990 (Rel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hemolysin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P16466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLYA_PROMI
                                                                                                              SUBCELLULAR LOCATION: Outer membrane.
MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMAINS
MAY BE RESPONSIBLE FOR PORE FORMATION.
SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA).
                                                                                                                                                                                 FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTER REQUIRES HPMB FUNCTION.
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 a license agreement (See
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                                   SEQUENCE FROM N.A. SEQUENCE FROM N.A.
                                                                                                                                  PATE - 2003 (Rel. 41, Last sequence up 28-FEB-2003 (Rel. 41, Last sequence up 28-FEB-2003 (Rel. 41, Last annotation putative surface-exposed virulence pro BIGA OR STM3478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
 Stojiljkovic I., Valentine I "Salmonella typhimurium rhs Submitted (MAR-1999) to the
                                                                                            Bacteria; Proteobacteria;
Enterobacteriaceae; Salmor
                                                                               NCBI_TaxID=602;
                                                                                                                       Salmonella typhimurium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
                                                                                                                     Local
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                                  422
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M64606; AAA27042.1;
M64606; AAA27043.1;
                                                                  17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a requires a license agreement (S
an email to license@isb-sib.ch).
                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94606; AAA27043.1; ALT_FRAME.
SG10437; bigA.
9; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pean Bioinformatics Institute. There are no restrictions non-profit institutions as long as its content is in and this statement is not removed. Usage by and for contents the statement is not removed.
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                               SGNGTTTNFAGD-----IAVSGGGTAIIIDGDNATIKNTGTSDISGAGSTGTVIDGNNAR
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-DTLLNTGATTNVTNDNVT-DDEKKRAASVKD---
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S., Layman D.
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                                                                                                                                                                                             VSGDSNAVDITGNVNISADYGQDDLAAGAPPLTGVVVGGNGNTVTLNGALNIDDNDLSAT
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                               -YAI----GYSSISDGGNWIIKGTASGNSRGHFGASASVG
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01-OCT-1994
                                                                                                                                                                                                                                                                                         Blaser M.J., Gotschlich E.C.;
J. Biol. Chem. 265:19372-19372(1990).

-I- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. THIS PROTEIN IS
CRITICAL FOR VIRULENCE.

-I- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
S-LAYER WITH HEXAGONAL SYMMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S-layer
SAPA.
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Blaser M T
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MEDLINE=91035477; PubMed=2229082;
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J. Biol. (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
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29, Last sequence update)
30, Last annotation update)
Surface array protein) (SAP)
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Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h E.C.;
of Campylobacter fetus.
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SEQUENCE
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P15320;
                                                                               STRAIN=SN8;
MEDLINE=88257037; PubMed=3290200;
                                                                                                                                                                                    01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last seq
01-NOV-1990 (Rel. 16, Last ann
                                                                                                      SEQUENCE FROM N.A., AND
                                 J. Bacteriol. 170:3177-:
                                                      marcescens.";
                                                                                                                                     Enterobacteriaceae; Serratia
                                                                                                                                               Bacteria;
                                                                                                                                                        Serratia marcescens
                                                                                                                                                                            Hemolysin precursor.
                                                                         Poole K., Schiebel
                                                                                                                           NCBI_TaxID=615;
                                                              Poole K., Schiebel E., Braun V.;
Molecular characterization of the hemolysin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
   FUNCTION: CELL-BOUND
             DEFINED
                       CELL MEMBRANES
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                                                                                                                                                                                                                                                                                                                                                                                    VSLGAGADAPTLSVDG--DALNVGS-KKDNKPVRITNVAPGVKEGDVTNV----AQL---
                                                                                                                                                                                                                                                                                                                                                                                                                                               FVGTTLTEGSVIDAPGNDTIAMKSAALTSANFTMIKNIENVAISDAVATADLSSSAFKNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGPKHLYSSKRRYCKFKRAAAKVKLNTTAATDQTVTLKANATDNSLEFDSATAKTTSVTA
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                                                                                                                                              Proteobacteria;
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933 AA;
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                    170:3177-3188(1988).
BACTERIAL HEMOLYSINS
RANES AND CAUSE CELL F
                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96757
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                                                                                                                                                                                      Last sequence up
                                                                                                       SEQUENCE
   HEMOLYSIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WW;
                                                                                                                                              Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 170;
Pred. No. 0
                                                                                                                                                                                                                                PRT;
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                     S ARE EXOTOXINS THAT AS RUPTURE BY MECHANISMS
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   WHICH
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                                                               determinant of
                                                                                                                                               Enterobacteriales;
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   HEME - IRON
                      MS NOT
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                                                                Serratia
                       CLEARLY
   FROM
                                  BLOOD
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                                                              RESULT 8
OMPB_RICRI
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Best Local Sim
Matches 125;
OMPB_RICRI
Q53047;
30-MAY-2000
30-MAY-2000
16-OCT-2001
Outer membra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR;
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   membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1608 AA;
(Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 40, Last annotation updat
ane protein B precursor (168 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A28182.
                                                    STANDARD;
                                                                                                                                              -GSAG-
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hemolysis; Toxin; Outer membrane; SIGNAL 1 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M22618; AAA50323.1; -.
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SUBCELLULAR LOCATION: Outer membrane.
SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 22.3
25; Conservative
KDAIYQGTALNGGRGKTAVNA
                                                   ---IIKGTASGNSRGHFGASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KAGWRMKTTTANG----QTGQADKFETVTSGTNVTFASGKGTTATVSK------DDQGNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRDSEKTTRTENSA--SSLSGGSVKLKAEKDVTFSGSKLVADKGDASVSGNKVSFLAADD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F-----LSADTKTTTVNVE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDARTGTAFNITSSSHKADNSYQSSTASEL------KSDTNLTLVSHKDADV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHASELTSGGTLRL----NGQQGVTITGSKARGQKGGEVTA-THGGLRID-NALSTTVDK
                                                                                                                                                                                                                                                            NKPVRITNVAPGV----KEGDV----TNVAQLKGVAQNLN------
                                                                                                                                                                                                                                                                                                                                                                ITRNGKNIDIATSMTPQFSSVSLGA------GADAPTLSVDGDALNVGSKK--D
                                                                                                                                                                                                                                                                                                                                                                                                                   ----INARDKLTQQGAQHSVGGAYQENAAGVDHLAAADTASTTTTKTDVGVNI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS--TDEGEGLVTAKEV--IDAVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGSQVASGGELSVESKTGNINVKAAERQQNIDEQKTALTVNGYAKEAGDKQYRAGLRIEH
                                                                                                                                                     RAGIAQAIATAGLVQAYLPGKSMMAIG----GGTYRGEAGYAIGYSSISDGGNW-----
                                                                                                                                                                                                        SSQAVVSSVQAGSIDINAKGEVRDQGTQYQASKG-AVNLTADSHRSEAAANRQDEQSRDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KTASNTEQTKIGGGFYYTGGIDK---LGSGVEAGYENNK-TQAQSSKAITSGSDVKGNLT
                                                                                                                                                                                                                                                                                                                  -GANVDYSAVTRPVERAVGKAAKLDATGVINDIGGIGAPNVGLDIGAQGGSSEKRSS
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                                                                                                      VRVYTTTGSDLTVDAKGEGGTQRSNSSASQAVTGSIDAANGINVNVK
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PRT;

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ion update) (168 kDa sı

surface-layer

protein)

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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning, expression and sequence analysis of the gene encoding to the surface-exposed protein of Rickettsia rickettsii."; Mol. Microbiol. 3:1579-1586(1989).

-i- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.

-i- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVEREI LAYER WITH HEXAGONAL SYMMETRY.

-i- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The 120 kilodalton outer membrane protein (rOmp B) of Rickettsia rickettsia is encoded by an unusually long open reading frame: evidence for protein processing from a large precursor."; mol. Microbiol. 5:2361-2370(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OMPB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Surface (rOmp B)
                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF03797; Autotransporter; 1.
TIGREAMs; TIGR01414; autotrans_barl; 2.
Antigen; S-layer; Cell wall.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90136087;
Gilmore R.D. Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR006315; Autotransport.
InterPro; IPR005546; Autotransporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X16353; CAA34403.1; -. PIR; S18227; S18227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 279-1654 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gilmore R.D.
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                                515
                                                               172
 224
                                                                                                                                                         400
                                                                                                                                                                                                                       340
                                                                                                                                                                                                                                                                                     114;
                                                                                                                                                                                        76
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                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                          VN----VESKDNG------KKTEVKIGAKTSVIKEKDGKLVTGKDK------GENGSST
                                                                                                                                                         TDFGNLAAQIKVPNAITLTGNFTGDASNPGNTAG-----VITFDANGTLESASADANVAV
                                                                                                                                                                                      DDEKKRAASVK--DVLNAGWNIKG--VKPGTTASDNVDFVRTYD---TVEFLSADTKTTT
                                                                                                                                                                                                                       NGKVATIDGQVYAKDMVIQSANATGQVNFRHIVDVGADGTTAFKTAASKVTITQDSNFGN
                                                                                                                                                                                                                                                 NGNKVNITSDTKGLNFAKETAGTNGDTTV-HLNGIGSTLTDTLLNTGATTNVTNDN--VT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
[Contains: 120 kDa surface-exposed protein (Surface prot
(120 kDa outer membrane protein ompB); 32 kDa beta pepti
KGTTATVSKDDQGNITVMYDV-----NVGDALNVNQLQNSGWN---
                                                          DEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVT-SGTNVTFASG------
                                                                                             TNNITAIEASGAGVVQLSGTHAAELRLGNAGSIFKLADGTVINGKVNQTALVGGALAAGT
                             ITLDGSATITGDIGNAGGAAALQRITLAN-----DAKKTLTLGGANIIGAGGGTIDLQA
                                                                                                                                                                                                                                                                                                                                                               1334
1181
                                                                                                                                                                                                                                                                                                                                              1654 AA;
                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=2515418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cieplak W. Jr., Policastro P.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=1724278;
                                                                                                                                                                                                                                                                                                                                                                1188
                                                                                                                                                                                                                                                                                                                                                                                 1654
                                                                                                                                                                                                                                                                                                 7.1%;
22.1%;
                                                                                                                                                                                                                                                                                                                                                168184 MW;
                                                                                                                                                                                                                                                                                  59;
                                                                                                                                                                                                                                                                                               Score 166.5; D
Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                             120 kDa SURFACE-EXPOSED PROTEIN.
32 kDa BETA PROTECO
                                                                                                                                                                                                                                                                                                                                                               POLY-THR.
                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                D7AB70FB7087F618 CRC64;
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                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                  214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Usage
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                                                                                                                                                                                                                                                                                                                 1654;
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-LDSKAVA-
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RESULT 9
ICEN_XANCT
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Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1990
01-NOV-1990
16-OCT-2001
                                                                        InterPro; IPR000258; Ice_nucleatn.
pfam; pF00818; Ice_nucleation; 81.
PRINTS; PR00327; ICENUCLEATION;
PROSITE; PS00314; ICE_NUCLEATION;
                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                     This
                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                            <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                     +
                                                                                                                                                                                                                                                                                                                                                                                                                                Xanthomonas campestris pv. translucens.";
mol. Gen. Genet. 223:163-166(1990).
-i- FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE
                                                                                                                                 EMBL; X52970; CAA37140.1;
HSSP; P06620; 1INA.
                                                                                                                                                                                                                                                       between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhao J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91080859; PubMed=2259339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-X56S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xanthomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xanthomonas campestris (pv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P18127;
                                                           Ice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Conserved repetition in the ice nucleation gene inaX from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ice nucleation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ICEN_XANCT
                                              nucleation;
UENCE 1567
                                                                                                                                                                                                                                                                                                           CRYSTALLIZATION IN SUPERCOOLED WATER.
SUBCELLULAR LOCATION: OUTER membrane (By similarity).
DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS
OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A
REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE
NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF IC
SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
                                                                                                                                                                                                                                      European
                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                  FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Orser C.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNATFNGNTTIAAN-STLQIGGNYTADCVASADGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGGTIKLT-STQNNIVVDFDLAIATDQTGVVDASSLTNAQTLTINGKIGTIGANNKTLGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FNIGSSKTVLSNGNVAINELVIGNDGAVQFAHDTYLITRTTNAAGQGKIIFNPVVNNGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGSFVFNAGGTNIVS-GTVGGQQGNKFNTV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVRIT----N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                              Repeat; Outer membrane.
AA; 152548 MW; C8B451D959ECAD63 CRC64;
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40,
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 7.1%;
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translucens)
Score 166;
Pred. No. 0.
                                                                           57.
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               DB 1; Length 1567;
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                                                                                                                                                                                        http://www.isb-sib.ch/announce/
                                                                                                                                                                                                           Usage
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Matches

Similarity

Conservative

69;

Mismatches

Indels

, 88

18;

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RESULT 10
OMPB_RICCN
ID OMPB_RICCN
ID OMPB_R
AC Q9KKA3
DT 16-OCT
CSURFA
CSURFA
CSURFA
RICKET
OC STRAII
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                                                                                                                                                                                                                                                                                                                                Samson D.,
Raoult D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9KKA3; Q9KK98; Q9XC45;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-DCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
(Surface protein Surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide
                  Submitted
                                                                                                                                                                                                                                                                                                                                             MEDLINE=21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiffren
Samson D., Roux V., Cossart P., Weiss
                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Malish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OMPB OR RC1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OMPB_RICCN
                                                                       Stenos
                                                                                       STRAIN=Malish
                                                                                                                                                                                                                    STRAIN-Indian tick typhus, and Malish MEDLINE-20393643; PubMed-10939649;
                                                                                                                                                                                                                                                        SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rickettsiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rickettsia conorii.
                                                                                                             SEQUENCE
                                                                                                                                                                          "Phylogenetic analysis of members
                                                                                                                                                                                                                                                                                          Mechanisms of evolution in science 293:2093-2098(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=781;
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os J., Walker D.;
os J., Walker D.;
rickettsial outer membrane protein A and B genes of Rickettsia rickettsia of the spotted fever group ralis, the most divergent rickettsia of the spotted fever group itred (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1094
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                                                                                            OF 353-1655
alish 7;
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                                                                                                                                            the outer-membrane
t. Evol. Microbiol.
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                                                                                                                                                                                                                                                                                                                                                                                                        1 N.A.
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                                                                                                                                                                                                                                                        FROM
                                                                                                          FROM
                                                                                                                                                                                                                                                N.A.
                                                                                                          N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alphaproteobacteria;
                                                                                                                                                                                                                                                                                                             Rickettsia
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                                                                                                                                          protein rOmpB (ompB)."; 50:1449-1455(2000).
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Weissenbach
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ch J., Claverie
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                                                                                                                                                                                                                                                                                                                                                                    Barbe
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                                group.
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the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
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or send an email to license@isb-sib.ch).
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InterPro; IPR005546; Autotransporter.
Pfam; PF03797; Autotransporter; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM I LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).
SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: THE 32 KDA BETA PEPTIDE MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; AE008659; AAL03623.1;
; AF123721; AAF34124.1;
; AF123726; AAF34129.1;
; AF149110; AAC39533.1;
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                                                                                              STDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVT
                                                                                                                    TNNITAIEASGAGVVQLSGTHAAELRLGNAGSVFKLADGTVINGKVNQTALVGGALAAGT
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                                                                                                                                                                                TDDEKKRAASVKD---VLNAGWNIKGVKPGTTASDNVDFVRTYD---TVEFLSADTKTTT
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12 Complete proteome.
120 kDa SURFACE-EXPOSED PRO
32 kDa BETA PEPTIDE.
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3 -> S (IN STRAIN INDIAN T)
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9 -> S (IN REF. 3).
10 -> R (IN REF. 3).
11 -> R (IN REF. 3).
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13 -> R (IN REF. 3).
14 -> R (IN REF. 3).
15 -> R (IN REF. 3).
16 -> S (IN REF. 3).
17 -> R (IN REF. 3).
18 -> R (IN REF. 3).
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Indels Length CRC64;

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                                                                                                                                                                                                                                                    "Evidence for proteolytic cleavage of the 120-kilodalton outer membrane protein of rickettsiae; identification of an avirulen mutant deficient in processing."; Infect. Immun. 60:159-165(1992).

-1- FUNCTION: THE 120 kDa SUFFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH WAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.

-1- FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS A MEMBRANE FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS A MEMBRANE SUBJECTURAL THIS BACTERIUM IS COVERED S-LAYER WITH HEXAGONAL SYMMETRY.

-1- SUBGELULIAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED S-LAYER WITH HEXAGONAL SYMMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein B precursor (168 Mas surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
(rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Wilmington;
MEDLINE=92114896; PubMed=1370573;
Ching W.M., Carl M., Dasch G.A.;
"Mapping of monoclonal antibody binding sites on CNBr fragments
the S-layer protein antigens of Rickettsia typhi and Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Wilmington;
MEDLINE-94040787; PubMed=8224886;
Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;
"Cloning and sequence analysis of the gene esurface layer protein of Rickettsia typhi.";
Gene 133:129-133(1993).
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Mol. Immunol.
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                          EMBĹ; L04661; AAB48987.1;
PIR; JN0896; JN0896.
                                                                                                                                                                            the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hackstadt T., Messer R., Cieplak W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTIFICATION OF CLEAVAGE SITE. MEDLINE-92104668; PubMed-1729180;
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                                                                                                                                                                            European Bioinformatics Institute.
                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way fied and this statement is not removed. Usage by and for commercial ties requires a license agreement (See http://www.isb-sib.ch/announce/end an email to license@isb-sib.ch).
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P35828; Q46015; Q9RFT2;
01-JUN-1994 (Rel. 29, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
5-layer protein (Paracrystalline surface layer prospection (Paracrystalline surface layer prospection).
Caulobacter crescentus.
Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteraceae; Caulobacteraceae
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CONFLICT
SEQUENCE
SEQUENCE FROM N.A., AND SEQUENCE OF 1
STRAIN-ATCC 1909 / CB15;
MEDLINE-93007489; PubMed-1393820;
GilChrist A., Fisher J.A., Smit J.K.;
"Nucleotide sequence analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
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Pfam; PF03797; Autotransporter; 1.
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1353 120 kDa SURFACE-EXPOSED PROTEIN
1645 32 kDa BETA PEPTIDE.
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Pred. No. 0.
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H -> N (IN REF.
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3 -> A (IN REF. 2).

3 -> S (IN REF. 2).

N; 0CB5641C7EB185EE C
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                                                                                     OF 1-21;
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Caulobacterales;

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Caulobacter

protein).

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574 401 -SIQLDGSAIITGDIG

528

341

473

292

---IQSANAGGQV

245 366 203 -GKL----

158

255

121

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Cell wal
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                                                                                                                                                                                                                                                                                                                                                                                          "The Caulobacter crescentus paracrystalline S-layer protein is secreted by an ABC transporter (type I) secretion apparatus.";
J. Bacteriol. 180:3062-3069(1998).
-I- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. PROBABLY ACTS AS PHYSICAL BARRIER TO PARASITES AND LYTIC ENZYMES.
-I- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A :
                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Fisher J.A., Smit J.K., Agabian N.;
"Transcriptional analysis of the major Caulobacter crescentus.";
J. Bacteriol. 170:4706-4713(1988).
                                           PRINTS;
                                                                                                                                                   EMBL; AF062345; AAC38665.2; EMBL; AF193063; AAF19365.1;
                                                                                                                                                                                               or send an
                                                                                                                                                                                                                                                           the
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                                                                                      HSSP; P22629; 1SWC.
                                                                                                                                   EMBL; AE005779; AAK22991.1;
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MEDLINE-98292737;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-313 FROM N.A., AND SEQUENCE OF STRAIN-ATCC 19089 / CB15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
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                                                                           [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gle W.H., Awram P.A., Nomellini J.F., e secretion signal of C. crescribe color of the mol. C-terminal 82 amino acids of the mol. mitted (OCT-1999) to the EMBL/GenBank,
                                                                                                                                                                                                                                                        ween the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                LAYER WITH HEXAGONAL SYMMETRY. SECRETED (TYPE I) SECRETION APPARATUS.

MISCELLANEOUS: THE CALCIUM BINDING OF TH SURFACE ATTACHMENT BY IONIC BRIDGING BET
                                                                                                                                                                                                                                                                                                                   SPECIFIC MEMBRANE-ASSOCIATED OLIGOSACCHARIDE.
                                                                                                                     A48995; A48995.
                                          Pro; IPR001343; Hemlysn_Ca_bind PF00353; hemolysinCabind; 3. S; PR00313; CABNDNGRPT.
                                                                                                                                                                                            requires a license agreement (S
an email to license@isb-sib.ch).
                                                                                                                                                                                                                           and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smit J.K.;
                          S-layer;
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AA;
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PubMed=9620954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=3049545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=11259647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / CB15;
                          Calcium-binding; Complete proteome
98001 MW;
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RESULT 13
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Best Local S
Matches 129
                                                   SEQUENCE FF
STRAIN=K12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YPJA_ECOLI STANDARD; PRT; 15
P52143; P76610; P77017; P77019;
01-OCT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                               Gregor J., Davis N.W., Kirkpatrick H.A., Goeden
                                                                                                                                                                                                                       Blattner F.R., Plunkett G. III, Bloch C.A., Riley M., Collado-Vides J., Glasner J.D., R
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical outer membrane
                         MEDLINE=97349980;
                                                                                                                             Science
                                                                                                                                                                                                                                                                                                                                                                                                  Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YPJA OR B2647
                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=562;
                                                                                                                          complete genome sequence complete 377:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89
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                                                                                                                                                                           Shao Y.;
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                                                                            FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TKAIYMGAGDDTVTVSSATLGAGGSVNGGDGTDV-----LVANVNGSSFSADPAFGGFET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDALNYGSKKDNKPYRITNYAPG--VKEGDYTNYAQLKGVAQNLNNRIDNYD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGWRMKTTTANGQTGQADKFETVTSG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAKTSV-IKEKDGKLV----TGKDKGENGSSTDEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VDGGANVTVASTGVTSGTT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LNAGWNI----KGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKI 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVGTEKLSFSAN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               {\tt LTATPTANT} - {\tt LTLNVNGLTTTGAITDSEAAADDGFTTINIAGSTASSTIASLVAADATTL}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----ITDSAAASATTAGKIATVTLGSFGAATIDSSALTTVNL-SGTGTSLGIGR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                   coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GNARAG
PubMed=9205837;
H., Baba T., Ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -GSTLT-----DTLLNT---GATTNVT---NDNVTDDEKKRAASVKDV
                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.0%;
23.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -IAQAIATAGLVQ----AYLPGKSMMAIGGGTYRGEAGYAIGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 163.5;
Pred. No. 0.
                                                                                                                                                 of
     Hayashi
                                                                                                                                                 Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ypjA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
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     <u>~</u>
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                                                                                                                                                                                                                         Rode C.K., Mayhew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
     Inada
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                                                                                                                                                 coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -TNVTFASGKGTTATVSKDDQGN
                                                                                                                                                                                                                                                                                                                                                                                                                            Enterobacteriales;
                                                                                                                                                                                                  M.A., Rose D.J.,
  Τ.
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     Isono
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Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EcoGene; EG13213; ypjA.

InterPro; IPR006315; Autotransport.
InterPro; IPR005446; Autotransporter.
InterPro; IPR0034899; Pertactin.
InterPro; IPR003991; Pertactin_C.
Pfam; PF03797; Autotransporter; 1.
Pfam; PF03791; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Construction of a contiguous 874-kb sequence of the Escher - K12 genome corresponding to 50.0-68.8 min on the linkage analysis of its sequence features.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oshima T., Oyama S.,
Tagami H., Takahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Itoh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR01484; PRTACTNFAMLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamagata S., Horiuchi T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mizobuchi K., Mori H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Outer membrane (Potential). SIMILARITY: STRONG, TO BORDETELLA PERTACTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; U36840; AAA79815.1; ALT_SEQ.; AE000350; AAC75695.1; -
; D90889; BAA16514.1; ALT_INIT
;, D90890; BAA16518.1; ALT_INIT
A65044; A65044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Res. 4:91-113(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T., Kimura
                                                                                                                                                                                                                                                                                                                                                                                                                                    164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NNETDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                          IAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWII--KGTASGNS
                                                                                        INGGSQVVNEGGLAENSVLNDGGTLDVREKGSATGIQQSSQGALVATTRATRVTGTRADG
                                                                                                                                       LSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAG
                                                                                                                                                                                          GEQIVDGGST
                                                                                                                                                                                                                                    SGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPT
                                                                                                                                                                                                                                                                                    AVDTIINANGKMDVYGKDVGTVLNSAGTQTIYASATSDKANIKGGKQTVYGLATEANIES
                                                                                                                                                                                                                                                                                                                                  V--TFASGKGTTATVSKD----DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGS
                                                                                                                                                                                                                                                                                                                                                                                      GGEAKHVEQQSGGALIASTTSGTLIEGTNSYGDAFYIRNSEAKNVVLENAGSLTVVTGSR
                                                                                                                                                                                                                                                                                                                                                                                                                               KGENGSSTDEGEGLV----TAKEVIDAVNKAG--WRMKTTTANGQTGQADKFETVTSGTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGEANYVVLENTGE-LTVVAKTSAKNT-TIDTGGKLIVQKEAKTDSTRLNNGGVLEVQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKD :: | : | | : | | : : : | :: : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAIGSNISAGGSLIVYTGGIAHGVN-----QETGSALVANT-GAGTDIEGYNKLSHFTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --IGSTLT---DTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKG---VKPGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NATUTIINGGTQNINNYGIATGTNINSGTQNIK----SGGKADTTIISSGSRQVYEXDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGRO1414; autotrans_barl; 2.
TIGRO1414; autotrans_barl; 2.
cal protein; Outer membrane; Complete proteome.
1589 AA; 162774 MW; 0D006A9A32154596 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.0%;
19.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kitagawa M., Makino K., Miki T., Mitsuhashi N., H., Nakade S., Nakamura Y., Nashimoto H., Saito N., Sampei G., Satoh Y., Sivasundaram S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H., Takeda
-ANNILLANGGVLTVESDTSSDKTQVNMGGREIVKTKATATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALT_INIT.
ALT_INIT.
                                                                                                                                                                                       -EKTHINGGTQ-TVQNYGKAIN--TDIVSGLQQIMANGTAEGSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86;
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Pred. No. 0.2
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MEDILINE-91358349; PubMed=1679432;
Beliveau C., Potvin C., Trudel J., As
"Cloning, sequencing, and expression
Streptococcus faecalis autolysin.";
J. Bacteriol. 173:5619-5623(1991).
                                                                                                                                                                                                                        Hydrolase; Gly
Cell division;
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SEQUENCE FROM N.A.
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15-SEP-2003 (Rel. 42, Last annotation update)
Autolysin precursor (EC 3.2.1.-) (Peptidoglycan hydrolase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterococcus faecalis.";
Science 299:2071-2074(2003).
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Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI_TaxID=1351;
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                                                                                                                                                                                                     SIGNAL
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InterPro; IPR002482;
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TIGR; EF0799; -.
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MEDLINE=22550857; PubMed=12663927;
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SIMILARITY:
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SUBCELLULAR LOCATION: Secreted (Probable).
DOMAIN: LYSM REPEATS ARE THOUGHT TO BE INVOLVED
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SM00047; LYZ2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                                     Glycosidase; Bacteriolytic enzyme; Cell wall; ion; Septation; Repeat; Signal.
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                                                                                                                        influenzae: structure and localization.";
Mol. Microbiol. 13:863-873(1994).
-!- FUNCTION: BINDS HEME/HEMOPEXIN COMPLEXES.
-!- SUBCELLULAR LOCATION: Secreted.
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MEDLINE-95115556;
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                                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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L.D., Thomas S.E., Latimer J.L., Slaughter
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A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B A;Reference number: A81000; MUID:20175755; PMID:10710307
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A;Status: preliminary
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, K.E.; Eisen; Dougherty, Pizza, M.

Eisen, В

8

Rappuoli, R.; strain MC58.

193

63

123

253

183

313

373 243

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adhesin homolog HI1732 - Haemophilus influenzae (strain Rd KW20)
c;Species: Haemophilus influenzae
c;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Oct-1997
C;Accession: I64138
R;Feleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.;
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M
, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagu
                                                                                                                                         RESULT
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C;Barkhill, J; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Nature 404, 502-506, 2000
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A; Residues: 1-592 < PAR>
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Best Local S
Matches 420
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                                                                                                                                                                                                                  EAGYATGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                                                                                                                                      EAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                                                                                                                                                                                             GDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRG
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O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage,
Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,
hman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
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A; Residues: 1-298 <TIGR>
                                                                                                                                                                                                                                                                                           A; Contents: annotation
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91; Conserv
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                      IVGGASLTLSGINAGSHKITNVTAGTEDTDAVNFSQLK---
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A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Wartins
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
A; Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-2059 <SIM>
A; Cross-references: GB:AE003982; GB:AE003849; NID:g9106554; PIDN:AAF84338.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: The genome sequence of the plant pathogen Xylella fastidiosa A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: D82671
R;anonymous, The Xylella fastidiosa Consortium of
Nature 406, 151-157, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          surface protein XF1529 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:U32846; GB:L42023; NID:g1574588; PID:g1574589;
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                                                             SNELVITSHSSTSSVKTLANGESVVNRTVVNGD
                                                                                                                     NNETDLTS-VGTEKLSFSANG----NKVNITSDTKGLNFAKETAGTNGDTTVHLNGI---
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25.4%;
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Pred. No. 3.7e
23; Mismatches
                                                                                                                                                                                                                      Score 375.5; DB 2
Pred. No. 3.7e-12;
                                                                                                                                                                                         Mismatches
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Rd.
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SVSEAVDKGWTLTASGANG

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A; Molecule type: DNA
A; Residues: 1-1588 <STO>
A; Cross-references: GB:AE005174; NID:g12518349; PIDN:AAG58749.1;
A; Experimental source: strain O157:H7, substrain EDL933
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable adhesin Z5029 [imported] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli (c;Species: Escherichia coli (c;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: A86036
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                                                                                                                                                                              NNETDLTSVGTEKLSFSA----NGNK-----VNITSDTKGLNFAKETAGTNGDTTVHLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGH
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ADGQRQITNVAAGSADTDAVNVG-----QLKVTDAQVSQNTQSITNLDNR-VTNLDSRVT 1340
                                 VDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKG--
                                                                                                       T----GSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; F
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: H91188
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A;Residues: 1-1588 <HAY>
A;Residues: 1-1588 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB37903.1; PID:g13363955; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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Best Local Similarity
Matches 139; Conserv
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                                                                                                                                                                                                                                                                                                                                                             STEEDSLAVGTDSLAMGAKTIVNGDKGIGIGYGAYVDANALNGI--AIGSNAQ-VIHVNS
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                                 SGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDG
                                                                                                                                         NIENGIGDIVTTGSTKYFKTNTDGVDA--SAQGKDSVAIGSGSIAAAD--NSVALGTG-S
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                                                                                                     FASGKGTTATVSKDDQGNIT-VMYDVNVGDALNVNQLQNS---GWNLDSKAVAGSSGKVI
                                                                                                                                                                            --ENG----SSTDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVT
                                                                                                                                                                                                                ADGQRQITNVAAGSADTDAVNVG-----QLKVTDAQVSQNTQSITNLDNR-VTNLDSRVT
                                                                                                                                                                                                                                                                                                                         1----GSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDN
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Qy 263 DSKAVAG:	Db 938 SGLQNNT	Qy 207 DKFETVT	Qy 148 TSVIKEKI   1   Db 883 ASA	Db 829 TDAVNLS	780 V	Qy 46 TVHLNGIO	Db 720 SKGWNLL	<u>_</u>	Query Match Best Local Similari	A; Gene: XF1981	A; Reference number: A5 A; Contents: annotation C: Genetics:	A; Authors: da Silva, M.; Tsuhako, M.H.; Va	A; Authors: Martins, E, F.G.; Nunes, L.R.; C, Rodrigues, V.; Rosa,	J.D.; Junqueira, M.L. chado, M.A.; Madeira,	as-Neto, E.; Docena, of submitted to GenBank,	A; Experimental source: strain 9a5c R; Simpson, A.J.G.; Reinach, F.C.;	A; motecute type: DNA A; Residues: 1-1190 <sim> A; Cross-references: GB: AE004017:</sim>	A; Accession: A82615 A; Status: preliminary	A; Reference number: A: A; Note: for a complete	R; anonymous, The Xyle Nature 406, 151-157,	C; Date: 18-Aug-2000 #: C; Accession: A82615	A82615 surface protein XF198	RESULT 7	Db 1572 TNSQGEY	QY 445 GNSRGHF	Db 1512 SKLSGGI	Qy 385 GNARAGI	Db 1466	QY 336 DALNVGS
DSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSL  :  :    :	SGLQNNTVGTVSVGDASKGETRTVSNVADAKEATDAVNLRQLDRVAQDANRVV	DKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNL	TSVIKEKDGKLYTGKDKGENG-SSTDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQA	TDAVNLSQLNTAMAGSGAKSVHYYSTYDGGTQGGNYNGDGATGTRSIAVGVGTL	TVGSGVTLGSMGLVITDGPSVTSSGINAGSQKIINVAAGTAD	TVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAG-WNIKGVKPGTTA	SKGWNLLASGANSSNVAPGESVDLKNTDGNIVISKESGSNDVLFNLSSSLKLDKLTVGDT	GNKVNITSDTKGLNFA	core 360.5; DB 2; Length 1190; red. No. 1.2e-11;		19328	lada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; V	A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasal	Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuram. A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.	Briones, M.K.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, I as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000	strain 9a5c .nach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; A.	(M) 3:AE004017: GB:AE003849: NTD:q9107083: BTDN:AAE84783 1:		A; note: for a complete list of authors see reference number A59328 below	he Organization for	sequence_revision, 20-Aug-2000 #text_change 20-Aug-2000	[imported] - Xylella fastidiosa (strain 9a5c)		TNSQGEYSAALGAGIQW 1588	GNSRGHEGASASVGYQW 461	SKLSGGIASAMAMTGLPQAYIPGASMASIGGGTYNGESAVALGVSMVSANGRWVYKLQGS	GNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTAS	RISNVSAGVNNNDVVNYAQLKQSVQETKQYTDQRMVEMDNKLSKTE	PGVKEGDVTNVAQLKGVAQNI
322	990	262	1 206 7 937	. 882		104	779	7 45				.A.; da Silveir ettore, A.L.; 2	Miyaki, C.Y.; Palmieri, D.A R.V.; Sawasak	le, E.E.; Laigr	D.M.; Carrer, H		1: GSDDB:GN001			Nucleotide Sequen	00					8 1571	3 444	1511	384
Db 8:	Ωу 31	7	Db 7:	Qy 2:	<b>,</b> L	Db 6	Qy 1	Db 5:		Qy	4	Qy	Query Match Best Local Matches 15	A;Gene: sapB	A; Molecule t A; Residues: A; Cross-refe	A; Accession A; Status: p:	A; Authors: A; Title: Co	, S.; Moule Nature 413,	C;Accession: R;Parkhill, th, T.; Conn	thi	probable au C;Species:	RESULT 8	Db 1137	Qy 4	Db 1077	Оу 3:	Db 1017	Qy 3:	Db 9
842 QSITNLNTQVSNLDTR	305 KNI	85 DYTAYNMDTPQNSVGE	725 SLAMGAKTIVNADAĞI 256 QNSGWNLDSK	565 SEGTOGESTROITNVA  226 TTATVSKDDQG- :    :		605 GAGCLALGQNSSSSIE	165GENGSSTDE	552 SISQLAGDTSETYITE		69 VTNDNVTDDEKKRAAS	:     AFSANHG	15 SFSANGNKVNITSE	Match 15.2 Local Similarity 21.8 res 150; Conservative	В	le type: DNA es: 1-1107 <par> references: GB:AL51338</par>	on: AC0976 preliminary	parry, C.; Quail, N mplete genome seque	Nature 413, 848-852, 2001	: AC09/6 J.; Dougan, G.; Ja nerton, P.; Cronin,	this species has also 09-Nov-2001 #sequence_	autotransporter sapB : Salmonella enterica		:   ::  :  :: 37 RGMTSVGVSSYRGQSA	မှ		GVKEGDVT	:   17 AAGVDATAIGVGATAS	323 GAGADAPTLSV	991 DNKIESLSEGQTF

M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, uence of a multiple drug resistant Salmonella enterica se MUID:21534947; PMID:11677608 3 (imported] - Salmonella enterica subsp. enterica serova
ca subsp. enterica serovar Typhi
co been called Salmonella typhi
a\_revision 09-Nov-2001 #text\_change 18-Nov-2002 V-----VESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDK--- 164 : | :| :| :| :| :| :| :| :| 491 .2%; Score 357; DB 2; Length 1107; .8%; Pred. No. 1.6e-11; 9 92; Mismatches 190; Indels 256; Gaps RVTNIENGIGDIVTTGSTKYFKTNTDGADANAQGADSVAIGSGSI 901 ENGTGVKYIRTNDNGLEGQ------DAYATGNGATAVGYDAVAS 604 SVKDVLNAGWNIKGVKPGTTASDNVDFV---RTYDT----- 116 DTKGLNFAKETAGTNG----DTTVHLNGIGSTLTDTLLNTGATTN 68 lames, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
lames, K.D.; Thomson, N.R.; Pickard, L.; White, N.; Farr ANGQTGQ-----ADKFETVTSGTNVTFASGKG 225 EGSIALGSGSTSNRAITTGIRETSATSDGVVIGYNTTDRELLGAL 664 EG----TAKEVIDAV 187 -----SSVSLGAGAD 327 EFSVGSEDGQRQITNVAAGSADTDA---VNVGQLKVTDAQVSRNT --AVAGSSGKVISGNVSPSKGKMDETVNINAG----NNIEITRNG 304 IGIGLNTLYMADAINGIAIGSNARANHANSIAMGNGSQTTRGAQT 784 ----NITVMYDVNVGDALNVN------QL 255 ADGSEAQDAVTVRQLQNAIGAVTTTPTKYYHANSTEEDSLAVGTD 724 82; PIDN:CAD03303.1; PID:g16504923; GSPDB:GN00176

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R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, I., M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barro
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il, M.; Rutherford, K.; Simmonds, M.;
Nature 413, 523-527, 2001
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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AH0110
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A; Residues: 1-658 < KI
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                                                                                                                                                                                                                                                                                                                           GEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGATTNVTNDNVTDDEKKRAASVK------DVLNAGWNIKGVKPGTTASDNVDFVRT
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                                              GIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRG
                                                                                                                                                                                           AGNNI-EITRNGKNIDI--ATSMTPQFSSVSLGAGADAP-----
                                                                                                                                                                                                                                                           DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGD----TTVHLNGIGSTLTDTLLN
                           GIASAMSMASLTQPYTSGSSMTTIGAASYRGQSALSLGVSSISDSGRWVSKLQASSNTQG
                                                                                                                          GSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQN----LNNRIDNVDGNAR-----A
                                                                                                                                                           NSSGLAKPSATGANSATGGAGSVASGNNSTAFGSGAKATAANSAALGANSVADRANSVSV
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                                                                                                                                                                                                                                                                                                                                                                                                                              ----GGGVKYFHANSTQPDSVASGTNSVAIGPASLASGNAALASG
                                                                                                                                                                                                                                                                                             ----KYSNASNTSSG-----TVSVGNTAT-----GETRTVSNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 328.5; DB 2;
Pred. No. 2.8e-10;
9; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                             ----AIGDGAAASA----DGSVAIGQGSGDNGRGVEN
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S.; Barrell,
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F90901
flagellin [imported] - Escherichia coli (C;Species: Escherichia coli C;Apecies: 18-Jul-2001 #sequence_revision 1f C;Accession: F90961
R;Hayashi, T.; Makino, K.; Ohnishi, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
A43855
high-molecular-weight surface-exposed protein C; Species: Haemophilus influenzae
C; Date: 10-Mar-1993 #sequence_revision 18-Nov-C; Accession: A43855
C; Accession: A43855
                                                                                                           RESULT
F90961
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTDTLLNTGAT-TNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTY 114
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                                                                                                                                                                                                                                                                            TAGLVQAYLPGKSMMAIG-----
                                                                                                                                                                                                                                                                                                           NATTGNVEITAQTGSILGGIESSSGSVTLTATEGALA-----VSNISGNTVTVTANSGA 1209
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                                                                                          Escherichia coli (strain 0157:H7,
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Pred. No. 0.0029;
1; Mismatches 199
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                                                         18-Jul-2001 #text_change 03-Aug-2001
        Kurokawa, K.; Ishii, K.
Shiba, T.; Hattori, M.;
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          Shinagawa,
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Han, a

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A;Title: Genome sequence of enterohemorrhagic Escherichia coli O1 A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: F85809
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-585 <STO>
A;Cross-references: GB:AE005174; NID:g12516024; PIDN:AAG56938.1; A;Experimental source: strain O157:H7, substrain EDL933 C;Genettcs:
A;Gene: flic
                                                                                                                                                                                    hypothetical protein flic [imported] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli (c;Species: Escherichia coli (c;Species: Escherichia coli (c;Date: 16-Feb-2001 *sequence_revision 16-Feb-2001 *text_change 14-Sep-2001 C;Accession: F85809 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Maller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apo
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C; Superfamily:
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A;Molecule type: DNA
A;Residues: 1-585 <HAY
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Nature 409, 529-533, 2001
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F90961
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AS-GKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSS-----
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Pred. No. 0.003;
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hypothetical protein 2 - Haemophilus ducreyi C;Species: Haemophilus ducreyi C;Species: Haemophilus ducreyi c;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change C;Accession: T31105 R;Ward, C.K.; Lumbley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, J. Bacteriol. 180, 6013-6022, 1998
                                                                                                                                                                  A;Cross-references:
C;Genetics:
                                                                                                                                                                                                       A; Molecule type: DN
A; Residues: 1-4919
                                                                                                                                                                                                                                                                              A; Title: Haemophilus ducreyi secretes a filamentous hemagglutinin-like A; Reference number: Z20984; MUID:99030326; PMID:9811662
                                                                                                                                                  A; Gene:
                                                                                                                                                                                                                                                               A; Accession: T31105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163
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                                  1 NNETDLTS------VGTEKLSFSANGNKVNITSDTKGLNFAKETAGT---NGDTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 NETDLTSVGTEKLSFSANGNKVN------ITSDTKGLNFAKETAGTNGDTTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKGENGSSTDEGEGI.VTAK-EVIDAVNKAGWRMKTTTANGQTGQAD-KFETVTSGTNVTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTEGALSEINNNLQRIRELTVQATTGTNSDSDLD-----SIQDEIKS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLNGIGSTLTDTL-----LNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGT
 NNQSKLSANNLKIKKVRDLNLNNSELSANNLTLNTSNNITLKNKSKFTAGNMTLNVTNNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YTVSYSVNKDNGSVTVAGYAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AS-GKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLGLNGFNVN-GKGTITNKAATVSDLTSAGAKLNTT----TGLYDLKTENTLLTTDAAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGK 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DMKALXKAASEGSDGASLTFNGTEYTIAKA---TPATTTPVAPLIPGGITYQATVSKDVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -ETKAAAATSSITFNSGVLSKTIGFTAGESSDAAKSYVDDKGGIT--NVAD
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                                                                                        8.3%;
22.0%;
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                                                                         66;
                                                                       Score 194.5; DB Pred. No. 0.045; 6; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 195;
Pred. No. 0.
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48 HLNGIGSTLTDTLLNTGATTNVT-----

----NDNVTDDEKKRAAS-----

84

615

TLNN-DSELAANNLTLNVTKNVTLNDASKLSANKLDLNVTDNVTLNSKSTLSAGELTFKK

Qy 4 TDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGI 52	A; Accession: 140711 A; Accession: A0711 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Status: preliminary A; Cross-references: EMBL: U25133; NID: g801999; PIDN: AAA79683.1; PID: g802000 C; Genetics: A; Gene: sapB Query Match Best Local Similarity 23.0%; Pred. No. 0.0061; Matches 118; Conservative 66; Mismatches 223; Indels 106; Gaps 22;	SULT 14 0711 pB protein pB protein Species: Ca Date: 16-A Accession: Dworkin, J. Biol. Chan Biol. Chan Biol. Segn Title: Segn Reference I	343 KKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNV	Db 779 TLNASGTFTNGNLTTVKTLDVGDIQNETNKGNLTVGEDLHIKSKTKITNDGK 831  Qy 274 VIS	Qy  85 VKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADT 124    1
Oy 167 NGSSTDEGEGLUTAKEVIDAVNKAGWRNKTTTANGQTGQADKFETVTSGTNVT 219	Qy  13 KLSFSAGKVNITSDTKCLNFAKETAGT	Ilminary pe: DNA -1910 <kur> -1910 <id a="" color="" of="" prop<="" property="" td="" the=""><td></td><td>Qy  35 APGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIG 414                                       </td><td>Db 499 ANATDNSLEFDSGTAKTTSVTASGSGKTLVIKGAEVETLVNIDTTAFNGAADVSF 553  Qy 201 GQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNS 258   </td></id></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur>		Qy  35 APGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIG 414	Db 499 ANATDNSLEFDSGTAKTTSVTASGSGKTLVIKGAEVETLVNIDTTAFNGAADVSF 553  Qy 201 GQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNS 258

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	Sear Job	Qy Db	Оу	В
	Search completed: October 6, 2003, 09:33:34	Dy 427 GYSSISDGGNWIIKGTASG 445  :   :    :      		Db 1154 GSSAGTG
	4		371 GVAQNLNURIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAI 426   : ::	DVYFTNVELNATAGNVSIYAETK 1183

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Result
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AAY27202
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Amino acid sequenc
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AAU06182
ID AAU
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M. catarrhalis	ABP71294	24	2139		383
M. catarrhal	AAB69136	22	2314		386.5
Haemophilus	AAE30477	24	298	0	443
Haemophilus	AAB23859	21	1104	.2	573
Haemophilus	AAB23856	21	1104		573
Neisserial o	AAB37832	21	116	23.1	600
Haemophilus	AAB23854	21	1002	6.	679
Haemophilus	AAB23857	21	1004	٥.	683
Amino acid s	AAY27201	20	245	0.	m
Haemophilus influ	AAB23855	21	679	0	m
Haemophilus	AAR99394	17	679	0	m
Haemophilus	AAR99393	17	2353	٠.	954.5
Haemophilus influ	AAB23860	21	2411	5	(n
Haemophilus	AAR99392	17	1098	œ	991
Haemophilus infl	AAB23858	21	1094	œ	991
N. meningitidis	AAU06184	22	407	σ,	2000.5
N. meningitidis	AAU06181	22	604	0	2098
N. meningitidis P	AAU06185	22	433		7
N. meningi	AAU06173	22	589	ς,	2254.5
A surface	AAY23745	20	589	5	25
Amino acio	AAY27203	20	592	<u>.</u>	2260
N. meningitidis	AAU06180	22	592	œ	2289
N. meningitidis	AAU06186	22	502	:-	2383
N. meningitidis H4	AAU06172	22	592	Ņ	2407
As	AAY23744	20	592	92.6	2407
N. meningitidis	AAU06178	22	598	Ψ	2418
A surface protei	AAY23738	20	598	ω ·	2418
N. meningitidis	AAU06177	22	598	Ψ	2427
≯ s	AAY23742	20	598	ω ·	2427
N. meningitidis	AAU06179	22	594	ω.	2442
A surface	AAY23739	20	594	ω	2442
N. meningitid	AAU06174	22	594	٠.	44
BASB029 amino aci	AAY57044	21	594	٠.	44
ace protei	374	20	594		44
ningitidis	AAU06176	22	599		2453.5
A surface protein	374	20	599	94.4	453.

## T 1 182 AAU06182 standard; Protein; 512 AA. AAU06182; 24-OCT-2001 (first entry) N. meningitidis PMC21 NhhA deletion mutant #1. Surface antigen NhhA; meningococcal disease; meningitis vaccine; mutant; mutein.

ALIGNMENTS

Neisseria mening Synthetic.	Neisseria meningitidis strain PMC21. Synthetic
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	/label= Mature_NhhA_deletion_mutant_#1
	<pre>/note= "Predicted mature protein, specifically</pre>
WO200155182-A1.	
02-AUG-2001.	
25-JAN-2001; 2001WO-AU00069.	1WO-AU00069.
25-JAN-2000; 2000US-0177917.	0US-0177917.

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RESULT 2
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Matches 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             meningitidis mutant polypeptides of the surface antigen NhhA (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence represents N. meningitidis strain pMC21 surface antigen while number of the present sequence represents N. meningitidis strain pMC21 surface antigen mutant #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                                                                    ATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVINVAQL
                                                                                                                                                                                                                  TNDNVTDDEKKRAASVKDYLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTV
                                                                        SISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                       KGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYS
                                                                                                                                    KGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYS
                                                                                                                                                                                                                                                                    NVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNK
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ilarity 100.0%;
Conservative (
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Pred.
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SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV

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TDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV

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Query Match
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14-JAN-1998;
01-SEP-1998;
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bacterial
                                                                                                                                                                                                                                                                                                                                                                   The invention provides proteins (AAYZ7201-245) from Neisseria meningitidis (Strains A and B) and nucleic acid sequences (AAY9123-167) encoding the proteins. Compositions comprising the protein, nucleic acid or antibody specific to the protein are useful as pharmaceuticals, e.g. a vaccine composition or a diagnostic composition. The composition is also useful for treating or preventing an infection due to Neisserial bacteria, especially Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnostic compositions meningitidis infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New protein and its nucleotide sequence, useful in vacc diagnostic compositions for treating and/or preventing
                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of N. meningitidis protein
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DB; AAX99124.
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                                                                                                                                                                                                                                                               1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANNE-----
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TDEGEGIVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
                                                  VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
                                                                                       GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
                                                                                                    GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
                                                                                                                                        NGTNFTYSLKKDETDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN
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infection; treatment.
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98GB-0000760.
98GB-0019015.
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                                                         Query Match
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                                                                                                           The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                        Claim
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immunoreactive po
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DB; AAX85798.
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                                                                 Similarity
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86.6%;
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Pred. No. 1.1e-150;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                               standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
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                                                                                                                                                 /note=
51..10
/label= C3
/note= "Conserved
189..210
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/note= "Variable
125..188
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121..124
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                                                                                                                                                                                                                                                                                                                                                 The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhha (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen Nhha from N. meningitidis strain PMC21 is 1 of 10 Nhha polypeptide sequences (AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New NhhA surface antigen polypeptides and polynucleotides Neisseria meningitidis, useful in producing vaccines for preventing broad spectrum of Neisseria meningitidis -
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            VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
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                                                               GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
                                                                                                    NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN
                                                                                                                                                      YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ
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VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
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230..236
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86.6%;
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Matches 511;
                                                                                                                                  The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
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N-PSDB; AAX85788.
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                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid sequence from
                                                                                                                                                                                                                                                                                                                                                           Nisseria meningitidis; n; treatment; prevent; a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLYTGKDKGENGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGIGSTLIDTLLNTGATINVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RITHVAPGVKEGDVTHVAQLKGVAQNLHNRIDHVDGNARAGIAQAIATAGLVQAYLPGKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VNINAGNNIETTRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETYTSGTNYTEASGKGTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QNGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV
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                                                                                                                                                                                                                                                                                                                         meningitidis
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                                     /note=
389
                                                                          /note=
123
/note=
269
                                                                                                                                                   /note=
108
                                                                                                                                                                                        /note=
98
                                                                                                                                                                                                                             /note=
92
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                 /note=
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                                                        "Encoded
                                                                                            "Encoded
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antibacterial drug.
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                   CGT"
                                                                                                                                                                                                                                               AAT"
                                                                                              ACA"
                                                                                                                                 AATC"
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282

SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV

301

102 181 162 241 222

VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS

TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV

300 281

360 341

TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV

GIGSTLIDTLLNTGATINVINDNVIDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF

101 180 161 240

221

NGSNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN

TDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN

YLDPVQRTVAVLIVNSDKEGTGEKEKVEEDSNWAVYFDEKGVLTAREITLKAGDNLKIKQ

120

54

55 61 55

MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANNE-----

MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL

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This is the Nisseria meningitidis BASB029 amino acid sequence from CC serogroup B strain H44/76. The BASB029 protein is homologous to the CC Haemophilus influenzae surface fibril (HSF) protein. The invention CC relates to BASB029 polynuclectide sequences (AAZ39864-Z39865) and CC polypeptide sequences (AAY57044-Y57045) and their immunogenic fragments. CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria CC meningitidis infection in a mammal. Compositions containing BASB029 polypuclectides and polypeptides are useful for generating an immune CC directed against BASB029 is useful in treating humans with Neisseria CC meningitidis disease. The polynuclectide is useful in the diagnosis of the stage of infection, type of infection, susceptibility to an CC infection which results from increased or decreased expression of the CC polynuclectide, and for therapeutic or prophylactic purposes, CC particularly genetic immunisation. Antibodies against BASB029 infections
Query Match
Best Local S
Matches 510
                                                                                                              polynucleotides and polypeptides are also useful for treating infections particularly bacterial infections. The protein is useful in the screening and development of antibacterial drugs. Fused recombinant protein is useful for the stimulation of the immune system of an organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptide from neisseria meningitidis useful treatment or prevention of bacterial infections in
                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9958683-A2
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 510;
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                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ39865
                                                                                                                                                                                                                                                                                                                                                                                                                                               Fig
                                                                                                  the
                                                                   591 AA;
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
                                                                                                  protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                               74pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-EP03255
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                 97.8%;
86.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  English
Score 2543.5; DB Pred. No. 3e-150; Mismatches
                                BB
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                                21;
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mammal
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                                Length
79;
                                  591;
 Gaps
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δõ Б QY Вþ Š 밁

В

180

101

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Query Match
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Matches 510
                                                                                                                                                              The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans the N. meningitidis surface glycoproteins can also be used to
                                                                                                              Sequence
                                                                                                                                                                                                                                   Claim 1; Page 104-106; 132pp;
                                                                                                                                                                                                                                                      Neisseria meningitidis surface meningitidis infections
                                                                                                                                                                                                                                                                                                                                       OQYU)
                                                                                                                                                                                                                                                                                                                                                                                        14-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                            24-JUN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Surface
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                                                                                                                                                                                                                                                                                                                   Jennings MP,
                                                                                                                                                                                                                                                                                                                                                                     12-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunoreactive
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DB; AAX85793.
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                                                                      il Similarity
510; Conserv
          55
                                                                                                                                meningitidis surface glycoproteins can also be used to tor treat N. meningitidis infection in humans, especially form of vaccines. The proteins and antibodies can also d to identify immunoreactive peptides.
                             1
                                                                                                                                                                                                                                                                                                                                       VIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; surface glycoprotein; infection;
                            MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANNE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
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                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                   Moxon
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                                                                                                                                                                                                                                                                                                                   ER,
                                                                               97.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria
                                                                                                                                                                                                                                                                                                                                                TTD
                                                                                                                                                                                                                                                                                                                   Peak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  591
                                                                     1;
                                                                     Score 2538.5; DB 2
Pred. No. 6.2e-150;
1; Mismatches 1;
                                                                                                                                                                                                                                   English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    meningitidis.
                                                                                                                                                                                                                                                                 proteins
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                                                                                                                                                                                                                                                                 treating
                                                                                        Length
                                                                                          591;
                                                                     79;
                                                                                                                                                                         humans
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RESULT 8
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ID AAUG
XX AAUG
XX AAUG
XX AAUG
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XX Neis
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FT Reg;
FT Reg;
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                                                                                                                                                                                                                                                                                               N. meningitidis
                                                                                                                                                                                                                                                                                                                   24-OCT-2001
                                                                                                                                                                                                                                                                                                                                      AAU06175;
                                                                                                                                                                                                                                                                                                                                                          AAU06175
                                       Region
                                                                                                                                                               Region
                                                                                                                                                                                                                                                       Neisseria meningitidis strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                           antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TDEGEGLYTAKEYIDAYNKAGWRMKTTTANGQTGQADKFETYTSGTNYTFASGKGTTATV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GIGSTLIDILLNIGATINVINDNVIDDEKKRAASVKDVLNAGWNIKGVKPGITASDNVDF
                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YLDPVLRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM
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                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                          NhhA;
                                                                                                                                                                                                                                                                                               EG329 surface antigen NhhA polypeptide sequence
        /label= C4
/note= "Conserved
230..236
                                        211..229
                                                                                                   /note= "Variable
125..188
                                                                                                                              /label= C2
/note= "Conserved
121 124
                                                                                                                                                                109.
                                                                                                                                                                                               /label= Ci
/note= "Conserved
                                                /label= V3
/note= "Variable
                                                                     /label= C3
/note= "Conserved
189..210
                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                         /label=
                                                                                                                                                                         note= "Variable"
                                                                                                                                                                                  /label= V1
                                                                                                                                                                                                                                                                                                                                                           Protein;
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                                                                                                                                                                                                                                                                          meningococcal disease;
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Best Local S
Matches 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                           meningitidis mutant polypeptides of the surface antigen NhhA (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding while-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain EG329 is 1 of 10 NhhA polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New NhhA surface antigen polypeptides and polynucleotides Neisseria meningitidis, useful in producing vaccines for preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peak
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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nes 510; Conserv
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                                                                                                                                                  GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
                                                                                                                                                                                                       NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN
                                                                                                                                                                                                                                                                                                                            MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANNE-----
                                                                                                                                                              GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
                                                                                                                                                                                                                                                         YLDPVLRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ
SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
                                                       TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
                                                                                                           VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
                                                                                                                                                                                                                                                                                                            MNETLRITWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL
                                                                                             VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
                                        TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
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                                                                                                                                                                                                                                                                                                                                                                                                                          591
                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention
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237..59
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/note= "
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86.3%;
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                                                                                                                                                                                                                                                                                                                                                                                  Score 2538.5; DB 2
Pred. No. 6.2e-150;
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                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                Claim 12; Fig 6; 91pp; English.
                                                                                                                                New NhhA surface antigen polypeptides and polynucleotides Neisseria meningitidis, useful in producing vaccines for t preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                          mutant;
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                                                                                                                                                                                                           (UYQU)
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                                                                                                                                                                                                                                                                                                                       Protein
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52..513
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                                                                                                                                                                                                                                                                                               /label= Mature_NhhA_deletion_mutant
/note= "Predicted mature protein, s
claimed in claim 12"
                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1..51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
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meningitidis mutant polypeptides of the surface antigen NhhA (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen.

The present invention

relates to

the isolation of novel

The present sequence represents antigen NhhA deletion mutant.

N. meningitidis strain

for

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DB 20;

Length

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Indels

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Gaps

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RESULT 10
AAY23743
ID AAY23743
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AC AAY23
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AC ASUF
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N-PSDB; AAX85795.
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                                                Jennings MP,
                                                                                                                                      12-DEC-1997;
                                                                                                                                                                       14-DEC-1998;
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                                                                                                                                                                                                                                                                      Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                          Surface
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                                                                                   UNIV
                                                                                                                                                                                                                                                                                                                         protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDMLLNTGATTNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKGVAQNLNNRIDNVNGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYLGEAGYAIGY
                                                                                                                                                                                                                                                                                                                                                            protein
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                                                                                   INNOVATION QUEENSLAND.
                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                  Moxon
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                                                                                                                                    97GB-0026398
                                                                                                                                                                      98WO-AU01031
                                                                                                                                                                                                                                                                                                         peptide
                                                                                                                                                                                                                                                                                                                          surface
                                                                                                                                                                                                                                                                                                                                                            of Neisseria
                                                    ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.5%;
95.3%;
                                                                                                     LTD
                                                                                                                                                                                                                                                                                                                          glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 2456.5; DB 2
Pred. No. 6.6e-145;
                                                                                                                                                                                                                                                                                                                                                            meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Å
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                                                                                                                     AAU06176
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497; Conserv
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                                                                                                                                                                                                                                                                                                                                        ASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKD
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                                                                                                                     standard;
                                                                                                                                                                                                                          AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                                                                                                                                                                                         KKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQ
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Pred. No. 1.2e-144;
4; Mismatches 11;
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                   polypeptide sequence
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Query Match
Best Local Similarity
                                                      The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhha (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding whid-type surface antigen. The present sequence representing the wild type surface antigen Nhha from N. meningitidis strain H38 is 1 of 10 Nhha polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                Claim
                                                                                                                                                                                                               New NhhA surface antigen polypeptides and polynucleotides Neisseria meningitidis, useful in producing vaccines for the preventing broad spectrum of Neisseria meningitidis.
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/note= "Variable
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237..243
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Matches
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N-PSDB; AAX85792.
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                                                                                                                                                                    Neisseria meningitidis
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Matches 495;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSKKDNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       meningitidis strain EG327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EG327 surface antigen NhhA polypeptide sequence.
                                                                                                                                                                     /label= V4
/note= "Variable
239..594
                                                                                                                                                                                                                                                                                       /note= "Variable 213..231
                                                                                                                                                                                                                                                                                                                                              /label= C3
/note= "Conserved region
191..212
                                                                                                                                                                                                                              /note= "Conserved region 232..238
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117..126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= V1
/note= "Variable
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/note= "Conserved region
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                                                                                                                                                                                                                                                                                                                             /label= v3
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Best Local :
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                                                                                                                              TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSKKDNK
                                                                                                                                                                                                        TVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE
                                                                                                                                                                                                                                                            KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 512
                                                       PVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPG
                                                                                                                                                                                     TVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE
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                                                                                                            TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVQRTAVVLSFRSDKEGTGEKEVTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE
                                   PVRITNVAPGVKEGDVTNVAQLKGVAQNLNNHIDNVDGNARAGIAQAIATAGLVQAYLPG
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83.3%;
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Pred. No. 2.3e-144;
6; Mismatches 11;
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Best Local Sim
Matches 495;
                                                                                                                                                                                                                                                                                                                                               The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis surface proteins useful for treating N. meningitidis infections  \begin{tabular}{ll} \end{tabular} \label{table_equation}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A surface protein of Neisseria meningitidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 95-97; 132pp; English.
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N-PSDB; AAX85791.
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                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                               Local Similarity
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160 DFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENG
                              181
                                                                                   121 NTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGDPTVH 180
                                            100 lngigstltdtllntgattnvtndnvtddekkraasvkdvlnagwnikgvkpgttasdnv 159
                                                                                                                                              61 PYQRTAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE 120
                                                                                                                                                                                                     1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLEATVQASANNE------
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| MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLEATVQANATDDDDLYLE
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                              LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV
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                                                                                                                 -------TDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVH
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Pred. No. 6.3e-144;
4; Mismatches 13;
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			540	458	480	398	420	339	360	279	300

Search completed: October 6, 2003, 09:22:25 Job time: 46.9684 secs

Total number

Maximum Minimum

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seq

length:

length: 2000000000

Database

Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1,

2: /ggn2\_6/ptodata/1,

3: /cgn2\_6/ptodata/1,

4: /cgn2\_6/ptodata/1,

5: /cgn2\_6/ptodata/1,

6: /cgn2\_6/ptodata/1,

Title: Perfect score:

US-09-771-382-23 2600 1 MNKIYRIIWNSALN

protein -

Copyright

GenCore (c) 1993

on:

Scoring table:

BLOSUM62 Gapop 10.0 ,

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5, Appli 5, Appli 36, Appl 33, Appli 4, Appli 47, Appli 6, Appli 6, Appli 6, Appli 15, Appli 15, Appli 15, Appli 26, Appli 26, Appli

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/Backfiles1.pep:*
US-09-377-155-21
US-09-369-974-21
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sequence
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Sequence
Sequence
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21, Appl
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32, Appli
31, Appli
32, Appli
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SEQ ID NO 21
LENGTH: 591
TYPE: PRT
ORGANISM: Neisseria meningitidis
US-09-377-155-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: PEAK, Ian Richard Anselm APPLICANT: JENNINGS, Michael Paul APPLICANT: MOXON, E. Richard TITLE OF INVENTION: NOVEL SURFACE ANTIGEN FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
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Best Local Similarity
Matches 512; Conserv
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US-09-669-974-3-3
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GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/09/377,155
PRIOR TILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
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US-09-669-974-21
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PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
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           TDEGEGIVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
                                                            VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
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 TDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETYTSGTNYTFASGKGTTATV
                                                VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
                                                                                               GIGSTLTDTLLNTGATTNYTNDNYTDDEKKRAASVKDYLNAGWNIKGVKPGTTASDNVDF
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SEQ ID NO 2
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GENERAL INFORMATI
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CURRENT FILING DATE: 1990-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: PEAK, Ian Richard Anselm APPLICANT: JENNINGS, Michael Paul APPLICANT: MOXON, E. Richard TITLE OF INVENTION: NOVEL SURFACE AN
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                                                            STDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETYTSGTNYTFASGKGTTAT
                                                                                             FVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLYTGKDKGENGS
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: POT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
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US-09-669-974-2
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US-09-669-974-2
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                                                                                                                                                                    FVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGS
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 VNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV
                                                               VSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDET
                                                                                                                            STDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTAT
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                                              VSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDET
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; TYPE: PRT
; ORGANISM: Neisseria
US-09-377-155-11
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PRIOR FILING DATE: 198-12-14
PRIOR APPLICATION NUMBER: GB 97
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
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CURRENT FILING DATE: 1999-08-19
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Pred. No. 2.2e-196;
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR PILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
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NUMBER OF SEQ ID NOS: 33
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US-09-669-974-11
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                ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM
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 ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM
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GENERAL INFORMATION:
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Matches 497
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PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 15
LENGTH: 599
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CURRENT FILING DATE: 1999-08-19
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                                                             KKDNKPYRITNVAPGYKEGDYTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQ 453
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CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-13-12
PRIOR FILING DATE: 1997-13-12
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
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497; Conservative
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             AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 512
                                                                     KKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQ
                                                                                                          KGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASG
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AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
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                                                   KDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQ
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Pred. No. 1.6e-189;
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RESULT

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RESULT 10 US-09-669-974-9 ; Sequence 9, Application ; Patent No. 6333173

GENERAL INFORMATION:

480

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420

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GENERAL INFORMATION:

APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1998-019
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR PILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 33
SOFTWARE: Patentin Ver. 2.0
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; LENGTH: 594
; TYPE: PRT
; ORCANISM: Neisseria meningitidis
US-09-377-155-9
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Best Local S
Matches 495
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                                                       TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSKKDNK 398
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KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
             KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
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Pred. No. 3.6e-189;
6; Mismatches 11;
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RESULT 11
US-09-377-155-7
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; Patent No. 6197312
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CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
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Best Local S
Matches 495
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APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
  APPLICANT:
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SOFTWARE: PatentIn Ver. 2.0
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ORGANISM: Neisseria
09-669-974-9
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|MKIYRIIWNSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTDDDDLYLE
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PEAK, Ian
JENNINGS,
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83.3%; Pred.
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US-09-669-974-7

Sequence 7, Application US/09669974
Patent No. 6333173
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128

NUMBER: US/09/669,974

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US-09-377-155-7
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PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 594
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Best Local :
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TITLE OF INVENTION: NOVEL SURFACE ANTIGE
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
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TYPE: PF
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VENTION: NOVEL SURFACE ANTIGEN
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83.3%;
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Pred. No. 1.3e-188;
4; Mismatches 13;
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180 95 54 60 54

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RESULT 13
US-09-377-155-13
; Sequence 13, Application
; Patent No. 6197312
; GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Neisseria
US-09-669-974-7
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PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-13-12
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                                           APPLICANT: PEAK, Ian Richard Anselm APPLICANT: JENNINGS, Michael Paul APPLICANT: MOXON, E. Richard TITLE OF INVENTION: NOVEL SURFACE ALFILE REFERENCE: 065064/0128
                  CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
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    APPLICATION NUMBER:
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    PCT/AU98/01031
                                                            SURFACE ANTIGEN
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Pred. No. 1.3e-188;
4: Mismatches 13;
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; ORGANISM: Neisseria
US-09-377-155-13
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US-09-669-974-13
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; Patent No. 6333173
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                                                                                                GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
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CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
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PRIOR APPLICATION NUMBER: GB 9
PRIOR FILING DATE: 1997-12-12
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Sequence 5. Application US/09377155

Patent No. 6197312

GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 06504/0128

CURRENT APPLICATION NUMBER: US/09/377,155

CURRENT APPLICATION NUMBER: PCT/AU98/01031

PRIOR APPLICATION NUMBER: PCT/AU98/01031

PRIOR APPLICATION NUMBER: GB 9726398.2

PRIOR APPLICATION NUMBER: GB 9726398.2

PRIOR FILING DATE: 1997-12-12

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 5
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; TYPE: PRT
; ORGANISM: Neisseria
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Pred. No. 2.1e-187;
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Search completed: October 6, 2003, 09:35:40 Job time: 16.6919 secs

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Title:
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2427 2418	2441 2440 2427	2449 2446 2442	2474 2453.5 2450	2546 2538.5 2488	2550.5	Score
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## ALIGNMENTS

RESULT 1

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Peak I.R., Srikhanta Y., Dieckelman M., Moxon R.,
Peak I.R., Srikhanta Y., Dieckelman M., Moxon R.,
Pidentification and characterization of a gene end
membrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ data
EMBL; AF226375 AAF42524.1; -.
REMBL; AF226370; AAF41395.1; -.
REMBL; AF226370; AAF42519.1; -.
REMBL; AF226370; AAF42519.1; -.
REMBL; AF226374; AAF42523.1; -.
REMBL; AF256374; AAF64523.1; -.
REMBL; AF256311; AAK68872.1; -.
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rPro; IPR005594;
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                                                                                          SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
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Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti B.
A Ratti G., Santhni L., Savino S., Scarselli M., Storni E., Zuo P.,
A Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
A Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
A Moxon E.R., Grandi G., Rappuoli R.;
T "Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
R EMBL, AF226366, AAF42515.1;
R Pfam; pF03895; YadA;
R Pfam; pF03895; YadA;
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C SEQUENCE 591 AA; 62113 MW; 533453CAE5A91E1F CRC64;
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01-OCT-2002 (TrEMBLrel. 2
Outer membrane protein.
NHHA.
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Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF125375; AAK09243.1; -.
InterPro; IPR005594; YadA.
Pfam; PF03895; YadA; 1.
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Bacteria; Proteobacteria;
Neisseriaceae; Neisseria.
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Peak I.R., S
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Pred. No. 2.6e-100;
0; Mismatches 1;
PRT;
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Q9JPS6;
Q9JPS6;
01-OCT-2000
01-OCT-2000
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF157606; AAK68867.1;
InterPro; IPR005594; YadA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria meningitidis.
Bacteria; Proteobacteria;
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01-DEC-2001 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
Nhha outer membrane prot
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NCBI_TaxID=487;
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15, 15,

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A Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,

Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,

A Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

A Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

A Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

A Hood D. W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

A Moxon E.R., Grandi G., Rappuoli R.;

"Identification of Vaccine Candidates Against Serogroup B

Meningococcus by Whole-Genome Sequencing.";

Science 287:1816-1820(2000).

EMBL; AF226371; AAR42520.1; -.

Pfam; PF03895; YadA; 1.
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NCBI_TaxID=487;
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Pred. No. 7.6e
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01-OCT-2000 (TrE
01-OCT-2000 (TrE
01-OCT-2002 (TrE
Outer membrane;
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Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,

Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti i;

Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

Moxon E.R., Grandi G., Rappuoli R.;

"Identification of Vaccine Candidates Against Serogroup B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Meningococcus by Whole-Genome Sequencing."; Science 287:1816-1820(2000).
EMBL; AF226378; AAF42527.1; -.
InterPro; IPR005594; YadA.
Pfam; PF03895; YadA; 1.
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Neisseriaceae; Neisseria.
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                                                                    DDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNI
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(TremBLrel 15, Last seq
(TremBLrel 22, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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84.7%;
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Pred. No. 2
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C Q9JPR8

C Q9JPR8

T 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Outer membrane protein GNA992 (NhhA outer membrane f

GN GNA992 OR NHHA.

OS Neisseria meningitidis.

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriaceae; Neisseria.
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Best Loc
Matches
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MEDLINE=201756; PubMed=10710308;

Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.

Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti

Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

Hood D.W., Jeffiles A.C., Saunders N.J., Granoff D.M., Venter C.,

Moxon E.R., Grandi G., Rappuoli R.;

"Identification of Vaccine Candidates Against Serogroup B

Meningococcus by Whole-Genome Sequencing.";

Science 287:1816-1820(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings "Identification and characterization of a gene encoding a nembrane protein of Neisseria meningitidis."; Submitted (JUN-199) to the EMBL/GenBank/DDBJ databases.
EMBL; AF226383; AAF42532.1; -.
EMBL; AF157608; AAK68869.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=H38;
Peak I.R.,
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                                                                                          ASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKD
                                                                                                                                                                                                                                                                                               KNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNG
                         KGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSK
                                                                                                                                                                                                                                                                                                                       DTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTT
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KGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSK
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Pred. No. 2.2e-9
4; Mismatches
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Nuti S.,
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Best Local S
Matches 496
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Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.

Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti

Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.

Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.

Moxon E.R., Grandi G., Rappuoli R.;

"Identification of Vaccine Candidates Against Serogroup B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9JPS2;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Meningococcus by Whole-Genome Sequencing. Science 287:1816-1820(2000). Science 287:26379; AF226379; AF226379; AF2667642528.1; -.
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Bacteria; Proteobacteria;
Neisseriaceae; Neisseria.
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01-OCT-2002
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                                                                             SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTFASGNGTTA
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(TrEMBLrel. 15,
(TrEMBLrel. 22,
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Pred. No. 3e-9
3; Mismatches
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Q93QY4;
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Bacteria; Proteobacteria;
Neisseriaceae; Neisseria.
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EMBL; AF226376; AAF42525.1; --

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(C STRAIN-BZ198, and 297-0;

(X MEDLINE-20175756; Pubmed=10710308;

(X Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

(X Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

(X Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.

(A Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nutri

(X Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.

(X Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

(X Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.

(X Moxon E.R., Grandi G., Rappuoli R.;

(**Identification of Vaccine Candidates Against Serogroup B

(**Meningococcus by Whole-Genome Sequencing.";

Science 287:1816-1820(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9JPH7; PRELIMINARY;
Q9JPH7;
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                             Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennin Identification and characterization of a gene encoding membrane protein of Neisseria meningitidis."; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF226358; AAF42507.1; -. EMBL; AF226358; AAF42507.1; -. EMBL; AF256364; AAF42507.1; -. EMBL; AF256386; AAF42507.1; -. InterPro; IPR005594; Yada.

Pfam; PF03895; Yada.
Pfam; PF03895; Yada; 1. 436BDDED68263C5C CRC64;
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Bacteria; Proteobacteria;
Neisseriaceae; Neisseria.
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EMBL; AR226361; AAF44510.1; -.
InterPro; IPR005594; YadA.
Pfam; PF03895; YadA; 1.
SEQUENCE 592 AA; 61917 MW;
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Bacteria;
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MEDLINE=20175756; PubMed=10710308;
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Science 287:1816-1820(2000).
EMBL; AF226382; AAR42531.1; -. InterPro; IPR005594; Yada.
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Bacteria; Proteobacteria;
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 22, Last annotation updatane protein GNA992.
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                   Score 2440; DB 2;
Pred. No. 8.1e-96;
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                                                                                             STRAIN-NGH15;

(C STRAIN-NGH15;

(X MEDLINE-20175756; PubMed=10710308;

(A Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

(A Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.

(A Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.

(A Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti

(A Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.

(A Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

(A Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.

(A Moxon E.R., Grandi G., Rappuoli R.;

(A "Identification of Vaccine Candidates Against Serogroup B

(A Meningococcus by Whole-Genome Sequencing.";

(C STRAIN-NGH15;

(A Moxon E.R., Grandi G., Rappuoli R.;

(A 
  STRAIN=H15;
Peak I.R., Srikh
"Identification
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01-OCT-2000
01-OCT-2000
01-OCT-2002
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
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Bacteria; Proteobacteria;
Neisseriaceae; Neisseria.
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||NKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE
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Submitted (JUN-1999) to the EMBL
EMBL; AF226381, AAF42530.1; -.
EMBL; AF157607; AAK68868.1; -.
InterPro; IPR005594; YadA, ..
Pfam; PF03895; YadA, 1.
SEQUENCE 598 AA; 62763 MW; E
                                                                                                                                                         GNA992.
Neisseria meningitidis.
Neisseria, Proteobacteria,
Bacteria, Proteobacteria,
                 STRAIN=2996;
MEDLINE=20175756; PubMed=10710308;
Pizza M., Scarlato V., Masignani V., Giu
Comanducci M., Jennings G.T., Baldi L.,
Galeotti C.L., Luzzi E., Manetti R., Mar
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09JPTO;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Outer membrane protein GNA992.
                                                                                                                SEQUENCE
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) to the EMBL/GenBank/DDBJ databases
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Broeker M., Hundt E., Knapp B., Blair E., Mason T
Hood D.W., Jeffries A.C., Saunders N.J., Granoff
Moxon E.R., Grandi G., Rappuoli R.;
"Identification of Vaccine Candidates Against Ser
Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
EMBL; AF226359; AAF42508.1; -.
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PRELIMINARY SEQUENCE OF 53-78.  STRAIN-ML 308-225;  MEDLINE-89291704; PubMed-2661530; Caffrey P., Owen P.;  "Purification and N-terminal sequence 43, a unique protein complex associate Escherichia coli.";  J. Bacteriol. 171:3634-3640(1989).  [5] SEQUENCE OF 53-63. STRAIN-K12 / EMG2; MEDLINE-97443975; PubMed-9298646; Link A.J., Robison K., Church G.M.; "Comparing the predicted and observed	SEQUENCE FROM N.A. STRAIN-R12; MEDLINE=97251358; PubMed=9097040; Itoh T., Aiba H., Baba T., Fujila K., Kasai H., Kimura S., Kitakawa M., Kita Mizobuchi K., Mori H., Mori T., Motom Nashimoto H., Nishio Y., Oshima T., Sa Sivasundaram S., Tagami H., Takeda J., Yamamoto Y., Horiuchi T.; "A 460-kb DNA sequence of the Escheric corresponding to the 40.1-50.0 min reg DNA Res. 3:379-392(1996). [3] SEQUENCE FROM N.A. STRAIN-ML 308-225; Henderson I.R., Owen P.; Submitted (JAN-1997) to the EMBL/GenBa	STANDARD; PRT; 15614; P76360; P97241; Q4 95 (Rel. 31, Created) 97 (Rel. 35, Last sequency) 11 (Rel. 40, Last annother 12 precursor (AG43) (Fluff) 13 proteobacteria; Gammapro- periaceae; Escherichia 1562; 16617; PubMed=9278503; 1742617; PubMed=9178503; 1780M N.A. 1780M N.A	34 156 6.0 642 1 FLID_CAMJE 35 156 6.0 918 1 YMJB_CAEEL 36 155 6.0 504 1 FLIC_SALNA 37 155 6.0 504 1 FLIC_SALRO 38 155 6.0 575 1 FLA2_CAMJE 39 155 6.0 1153 1 PVDB_PLAKN 40 154 5.9 1196 1 ICEV_PSESX 41 153.5 5.9 1637 1 MRSP_STAAU 42 153.5 5.9 2358 1 YEBJ_ECOLI 43 153 5.9 504 1 FLIC_SALBU 44 153 5.9 504 1 FLIC_SALBU 45 153 5.9 1200 1 ICEN_PSESY 45 153 5.9 1200 1 ICEN_PSESY 46 153 5.9 1200 1 ICEN_PSESY 47 ALIGNMENTS
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"Antigen 43, a phase-variable bipartite outer membrane
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MEDLINE-92326638; PubMed-1625582;
Benz I., Schmidt M.A.;
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InterPro; IPR005546; Autotransporter.
InterPro; IPR004899; Pertactin.
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EMBL; D90794; BAA15197.1; AI
EMBL; X73295; CAA51730.1; AI
EMBL; A64905; A64905.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIJINE=94100243; PubMed=8274505;
Cartwright P.J., Timms M.W., Lithgow T., Hoej P.B., Hoog
Tan Escherichia coli gene showing a potential ancestral
to the genes for the mitochondrial import site proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blattner F.R., Plunkett G. III, Bloch C.A
Riley M., Collado-Vides J., Glasner J.D.,
Gregor J., Davis N.W., Kirkpatrick H.A., C
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Aiba H., Baba T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=K1
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                                                                                                                                                                                                                          Hypothetical
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Bacteria; Proteobacteria;
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SUBCELLULAR LOCATION:
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                     146;
                                       Similarity
                                                                                                                                                                                                                                              905; A64905.
EG11780; ydeK.
PS00013; PROKAR_LIPOPROTEIN;
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                                     8.2%;
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ALT_INIT.
ALT_FRAME.
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N -> K (IN REF. 3).
M -> S (IN REF. 3).
MW; 26A3A066FA19AD7D CRC64;
                   Score 214.5; DB :
Pred. No. 0.00093
2; Mismatches 250
                                                                                                                                                                       POTENTIAL.
HYPOTHETICAL LIPOPROTEIN YDEK
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C.K., Mayhew G.F.
n M.A., Rose D.J.,
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SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado-Vides J., Glasner J.D., Rc
Riley M., Davis N.W., Kirkpatrick H.A., Gov
                                                                                                                 Science [2]
MEDLINE=97251357; PubMed=9097039;
Aiba H., Babb T., Fujita K., Hayashi K., Inada T., Isono K.,
Kitagawa M.,
Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura
Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,
Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,
                                                                                                                                                                                                                                                                                                                     YDBA_ECOLI STANDARD; PRT; 2(

933666; P76087; P76088; P76856; P76857

01-FEB-1994 (Rel. 28, Created)

16-OCT-2001 (Rel. 40, Last sequence up

16-OCT-2001 (Rel. 40, Last annotation

Hypothetical protein ydbA.

TOBA OR B1401/B1405.
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                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammar
Enterobacteriaceae; Escherichia.
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nce 277:1453-1474(1997).
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6; P76857; P
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Goeden M.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochimie 73:1361-1374(1991).
-!- SIMILARITY: TO S.TYPHIMURIUM ORF NEAR CYSG
-!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moszer I., Glaser P., I
"Multiple IS insertion
Escherichia coli K-12."
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"A 570-kb DNA sequence of the k
corresponding to the 28.0-40.1
DNA Res. 3:363-377(1996).
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L; AE000237; AAC74467.1; ALT_SEO.
L; D90778; BAA15099.1; ALT_SEO.
L; D90778; BAA18880.1; ALT_SEO.
L; D90779; BAA18881.1; ALT_SEO.
L; D90779; BAA18881.1; ALT_SEO.
L; X62680; VOTA ANNOTATED_CDS.
Gene; EG11307; ydba.
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136; Conserv
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                 VSGDANTVNITGNVLVDKDKTADNAAEYFFDPSVGINVYGSDNNVTLDGKLTVVSDSEVT
                                            VDGDALNV--
                                                                                                                                                     MYDVNVGDALNV----NQLQNSGWN--LDSK-----AVAGSSGKVISGNVSPSKGKMDET
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01-APR-1990 (Rel. 14, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Outer membrane protein A precursor (19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anderson B.E., McDonald G.A., Jones D.C., Re "A protective protein antigen of Rickettsia repeated, near-identical sequences.";
Infect. Immun. 58:2760-2769(1990).
'- FUNCTION: ELLCITS PROTECTIVE IMMUNITY.
'- SUBCELLULAR LOCATION: CELL WALL. THIS BASILATER WITH HEXAGONAL SYMMETRY.
                                                    SEQUENCE
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SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB
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01-AUG-1990 (Rel. 1
01-AUG-1990 (Rel. 1
01-NOV-1990 (Rel. 1
                               Uphoff T.S., Welch R.A.;
"Nucleotide sequencing of the Proteus mirabilis calcium-independent hemolysin genes (hpmA and hpmB) reveals sequence similarity with the Serratia marcescens hemolysin genes (shlA and shlB).";
J. Bacteriol. 172:1206-1216(1990).
-i- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD -i- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
                                                                                                                                                                                                                                Proteus mirabilis.
Bacteria; Proteobacteria;
Enterobacteriaceae; Proteo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TEVKIGAKT----SVIKEKDGKL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --AASVLTLTNANAVLTGAVDNTTGGDNVGVLNLNGALSQVTGDIGNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NT-TGGDNVGVLNLNGALSQVTGDIGNTNSLATISVGAGTATLGGAVIKATTTKLTN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AG----LLQVQGGVVKANTINLTDNASAVTFTN--PVVVTGAIDNTG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----VTGKDKGENGSST-DEGEGLVT----AKEVIDAVNKAGWRMKTTTANGQTGQADK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       509
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CELL-BOUND HEMOLYSIN,
                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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15,
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                                                                                                                                                                                   SEQUENCE OF
                                                                                                                                                                                                                                                   Gammaproteobacteria;
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 WHICH RELEASES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
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PIR; A35140; A35140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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SUBCELLULAR LOCATION: Outer membrane.
MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMAINS MAY BE RESPONSIBLE FOR PORE FORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA).
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                                                                                                                                                            --AIATAGLVQAYLPGKSMMAIG------GGTYRGEAGYAIGYSSISDGGNWIIKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            {\tt TKPVKKAIEDGVNTTKPGNNTDLTKKYTARDAIANLSNLETPNVGVEVGIKGGGSQQ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LNFAKETAGT-NGDTTVH-----LNGIGS-----
                                                                                                                                DDASSVNGL----
                                                                                                                                                                                            ELNAGHNLTLQG-
                                                                                                                                                                                                                          RITNVAPGVKEGDVTNVAQLKGVAQNLNNRID------
                                                                                                                                                                                                                                                         DTHSESQSNVNGSANLKVGT--TPE--SKDYGGGFNAGTTHHSKEQTTAKVGTITGSQGI 1137
                                                                                                                                                                                                                                                                                     -----SVDGDALNVGSKKDNKPV
                                                                                                                                                                                                                                                                                                                                                                                   TTFHETKGGGQIGVSTK----TGSDITVAIKGEGQTTDNALMETKAKGSQFTSNGDISI
                                                                                                                                                                                                                                                                                                                                                                                                                  WRMKTTTANGQTGQADKFETVTSGTNVTFA-SGKGTTA----TVSKDDQGNITVMYDV
                                                                                                                                                                                                                                                                                                                                                                                                                                               SQTDSQAVSTSINAGKIDI-DSNNKL---HDQGTHYQSTQEGISLTANTHTSEATLDKHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDA-VNKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FYSTENKKQTDNTDTTISGGFSYTGGYDKYGSKADFQYDKQHTQTEYTKNRGSQTEYAGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSTETEQANSTISG-----ANVDLQANK--DVTFAGSDLKTTAGN---ASITGDNVA
                                                                                                                                                                                                                                                                                                                                                    NVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----KGVKPG---TTASDNVDF---VRTYDTVEFLS--ADTKTTTVNVE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTITANKDLLHEGASHHVEGRYQESGENIQHLAVNDSETSKTDSLNVGIDVGVNLDYSGV
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1577 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165869 MW;
                                                                                                                                                                                           -THLSSEQDIALNATNKVDLQSASSEHTEKGNNLSGGVQAGFGKKMT
                                                                                                                              -GSAQFAIGKQDEKSVSREGGT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82;
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Pred. No. 0.076; 
12; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEMOLYSIN
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                                                                                                                                                                                                                                                                                                                      ----KGK---TV-INAGGDLTLAQAT 1081
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Best Local S
Matches 136
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01-JUN-1994
01-OCT-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blaser M.J., Gotschlich E.C.;
J. BLO1. Chem. 265:19372-19372(1990).
-i- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. THIS PROTEIN IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Campylobacteraceae;
NCBI_TaxID=196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Campylobacter fetus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S-layer protein (Surface array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLAP_CAMFE P35827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; J05577; AAA23032.1; Cell wall; S-layer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.,
STRAIN=84-32 / 23D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91035477; PubMed=2229082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Surface array protein of structure.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blaser M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=90354448; PubMed=2387868;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRITICAL FOR VIRULENCE.
SUBCELLULAR LOCATION: CELL WALL.
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                                                                                                                                                                                                                                                                                                                      VFNGYEKVGFNVLGDIVSFATDASKSVNV--ETTGTITAFTAAGTGKVDVVAGKISALTA 347
                                                                                                                                                                                                                                                                                                                                                                                    LNAIFTAITRAALLTDQAELII-----TKRRTNVENINIISDL-----ETSGDF
                                GTTATVSK--DDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAG---SSGKVISGNV 330
                                                                                                                                                                                                                                                                                                                                                    TSVGTEKLSFSANGNKVNITSD-TKGLNFAKETAGT----
 GTTLTEGSVIDAPGNDTIAMKSAALTSANFTMIKNIENVAISDAVATADLSSSAFKNSVI
                                                              SGKTLVIKGAEVETLVN----IDTTAFNALQSVSFGKTGQGGKF-SVKTGTGDDKIEFV
                                                                                                                            PKHLYSSKRRYCKFKRAAAKVKLNTTAATDQTVTLKANATDNSLEFDSATAKTTSVTASG
                                                                                                                                                                                            AVENLTYKHATNYALNGGMDKLATYTLDNAALTAAIDI-----KSASTLNLINSSYNG
                                                                                                                                                                                                                                                         DSRTSVNLTATNDTITLTSANAATSVNLKQRQAKDATITSAMQQKYNNRRNRIATITSAT 407
                                                                                                                                                                                                                                                                                       NGDTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTD-----DEKKRAA-----
                                                                                                                                                            --------KKTEVKIGAKTSVIKEK------DGKLVTGKDKGENGSSTDEG
                                                                                                                                                                                                                          ----SVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVN-VESKDNG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S-layer.
933 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                             -LVTAKEVIDAVNKAGWRMKTTTAN---
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Campylobacter.
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Campylobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 176.5; DE Pred. No. 0.052; 4; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quence update)
notation update)
y protein) (SAP).
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STRAIN-Mailsh 7;
MEDLINE-21442074; Put
Ogata H., Audic S., I
Samson D., Roux V., (
  the Europuse by modified
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O9KKA3; Q9KC45;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Outer membrane protein B precursor (168 kba surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
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-!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
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Bacteria; Proteobacteria; Alp
Rickettsiaceae; Rickettsieae;
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by non-
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SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVER LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).

SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
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                                                                                                                                                                                                                               FUNCTION: THE
                  SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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EMBL; AF123721; AAF34129.1; -
EMBL; AF123726; AAF34129.1; -
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PF03797; Autotransporter; 1.
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                                                                                                                                                                                                                          FSSV----
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120 KDA SURFACE-EXPOSED PROTEIN.

120 KDA SURFACE-EXPOSED

3 kDA BETA PEPTIDE.

P -> A (IN STRAIN INDIAN TICK TYPHUS).

G -> S (IN STRAIN INDIAN TICK TYPHUS).

K -> N (IN STRAIN INDIAN TICK TYPHUS).

V -> A (IN STRAIN INDIAN TICK TYPHUS).

V -> A (IN STRAIN INDIAN TICK TYPHUS).

I -> V (IN STRAIN INDIAN TICK TYPHUS).

A -> T (IN STRAIN INDIAN TICK TYPHUS).

A -> T (IN STRAIN INDIAN TICK TYPHUS).

B -> C (IN REF. 3).

C -> S (IN REF. 3).

E -> D (IN REF. 3).

E -> D (IN REF. 3).

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                                                                                         TVGGQQGNKFNTVALDNGTTVKFLGNATFNGNTT
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617 317 559 264 507 216

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787 474 736 422 677

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RESULT 9
SLAP_CAUCR
                      "The Caulobacter crescentus paracrystalline S-layer protein is secreted by an ABC transporter (type I) secretion apparatus.";
J. Bacteriol. 180:3062-3063(1998).

-I- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY OF PROTEINS WHICH COAT THE SUFFACE OF BACTERIA. PROBABLY ACTS AS PHYSICAL BARRIER TO PARASITES AND LYTIC ENZYMES.

-I- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A LAYER WITH HEXAGONAL SYMMETRY. SECRETED BY AN ABC TRANSPORTER (TYPE I) SECRETION APPARATUS.

-I- MISCELLANBOUS: THE CALCIUM BINDING OF THIS PROTEIN MAY MEDIATE SURFACE ATTACHMENT BY IONIC BRIDGING BETWEEN THE S-LAYER AND A SUBCEPTION APPARATUS.
                                                                                                                                                                                                                                                                                                                                                                                                   Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Elsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White (Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; "Complete genome sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         **MEDIALE A., Fisher J.A., Smit J.K.; Gilchrist A., Fisher J.A., Smit J.K.; Rucleotide sequence analysis of the gene crescentus paracrystalline surface layer p Can. J. Microbiol. 38:193-202(1992).
                                                                                                                                                                                                                                                                                            SEQUENCE OF 19089 / CB15;
STRAIN-ATCC 19089 / CB15;
MEDLINE-89008089; PubMed=3049545;
Fisher J.A., Smit J.K., Agabian N.;
Fisher J.A., Smit J.K., Agabian N.;
                                                                                                                                                                                                                                                                                                                                                                                           Proc.
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P35828; Q46015; Q9
01-JUN-1994 (Rel.
                                                                                                                                                                                                                 STRAIN-ATCC 19089 / CB15;
MEDLINE-98292737; PubMed-9620954;
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STRAIN-ATCC 19089 /
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Bacteria; Proteobacteria;
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28-FEB-2003 (Rel. 41, Last annotation update)
S-layer protein (Paracrystalline surface layer protein).
                                                                                                                                                                                                                                                                            Caulobacter crescentus.";
J. Bacteriol. 170:4706-4713(1988).
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MEDLINE-21173698;
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             SPECIFIC
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              MEMBRANE-ASSOCIATED
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PubMed=11259647;
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PRINTS;
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HSSP; P22629; 1SWC.
TIGR; CC1007; -.
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AAQGSHNANGFTALQLGATAGATTFTNVAVNVGLTVLAAPTGTTTVTLANATGTSDV
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AAF19365.1; -.
AAK22991.1; ALT_INIT.
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CONFLICT
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MEDLINE=94040787; PubMed=8224886;
Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;
"Cloning and sequence analysis of the gene er
surface layer protein of Rickettsia typhi.";
Gene 133:129-133(1993).
                                                                                                                                                                                                                         TRANSMEM CONFLICT
                                                                                                                                                                                                                                                                             Antigen;
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Alp
Rickettsiaceae; Rickettsieae;
NCBI_TaxID=785;
                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hackstadt T., Messer R., Cieplak W., Peacock M.G.;
"Evidence for proteolytic cleavage of the 120-kilodalton outer
membrane protein of rickettsiae: identification of an avirulen
mutant deficient in processing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Mapping of monoclonal antibody binding sites the S-layer protein antigens of Rickettsia typprowazekil.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Wilmington; MEDLINE-92114896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (rOmp B) [Contains antigen) (120 kDa
                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                               TIGRFAMS;
                                                                                                                                                                                                                                                                                                                                    Pram;
                                                                                                                                                                                                                                                                                                                                                                    InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ching W.M.,
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(Surface protei
                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                               Match
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ect. Immun. 60:159-165(1992).

FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETISIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.

FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS A MEMBRANE SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED S-LAYER WITH HEXAGONAL SYMMETRY.

SIMILARITY: BELONGS TO THE RICKETISIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                               ; L04661; AAB48987.1; -.
JN0896; JN0896.
rPro; IPR006315; Autotransport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OR SLP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way the content is in the content in the content is in no way the content is in the content in the content in the content is in the content in the c
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[Contains: 120 k
TAQQAATTKSA--QNVVSKVNAGAAINDNDLSGVGSIDFTAAPSVLEFNLINPT----
                                     TKRASATVKTAVLATLLFATVQASANNETDLTSVGTEKLSFSANGNKVNITSDTKGLNFA
                                                                                                                                                                                                                                                                                                              3797; Autotransporter; 1.
TIGR01414; autotrans_barl; 1.
                                                                                                                                                                                                                                                                                                                                                IPR005546; Autotransporter.
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                                                                           Conservative
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21.2%;
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) (Cell surface antigen
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                                                                           81;
                                                                       Score 174.5;
Pred. No. 0.13
%1; Mismatches
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ace-exposed protein (Surface protein
protein ompB); 32 kDa beta peptide]
                                                                                        174.5;
No. 0.1
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                Gilmore R.D. Jr., Joste N., McDona "Cloning, expression and sequence 120 kD surface-exposed protein of Mol. Microbiol. 3:1579-1586(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
0uter membrane protein B precursor (168 kDa surface-layer pro
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rO
(rOmp B) [Contains: 120 kDa surface-exposed protein (Surface antigen) (120 kDa outer membrane protein ompB); 32 kDa beta p
                                                                                                                                                                             Gilmore R.D. Jr., Cieplak W. Jr., Policastro P.F. "The 120 kilodalton outer membrane protein (rOmp rickettsii is encoded by an unusually long open r evidence for protein processing from a large precedent Mol. Microbiol. 5:2361-2370(1991).
                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Rickettsiaceae; Rickettsia NCBI_TaxID=783;
                                                                                                         MEDLINE=90136087;
                                                                                                                              STRAIN=R
                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                             STRAIN=R
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 FUNCTION: THE 120 kDa SURFACE-EXPOSED STRUCTURAL PROTEIN WHICH MAY PLAY A RC
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                                                                                                                                               279-1654 FROM
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                                                                                      PubMed=2515418;
Joste N., McDonald G.
                                                                                                                                                                                                                                                                        PubMed=1724278;
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                                                                                                                                             N.A.
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Rickettsia r
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                                                                   the gene encoding
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                                                                                                                                                                                                                 F., Hackstadt T.;
p B) of Rickettsia
reading frame:
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                    A MAJOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; S1822/; S1822/.
InterPro; IPR006315; Autotransport.
InterPro; IPR005346; Autotransporter.
Pfam; PF03797; Autotransporter; 1.
TIGREAMS; TIGR01414; autotrans_bar1; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antigen; S-layer; Cell wall. CHAIN 1 1333
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SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED
LAYER WITH HEXAGONAL SYMMETRY.
SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
690
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                                                          631
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149; Conserv
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                                                                                                                       TIKLTSTQNNIVVDFDLAIA-TDQTGVVDASSLTNAQTLTINGKIGTIGANNKTLGQFNI
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                           AGIAQAIATAGLVQAYLPGK----SMMAIGGGTYRGEAGYA----IGYSSISDG
                                                          GSSKTVLSNGNVAINELVIG-NDGAVQFAHDTYLITRTTNAAGQGKIIFNPVVNNGTTLA
                                                                                         GSKK---DNKPVRITNVAPGVKEGDV-----
                                                                                                                                                    NIEITRNGKNI----DIATSMTPQFSSVSLGAGADAPTLSVDG
                                                                                                                                                                                     AGTITLDGSATITGDIGNAGGAAALQRITLANDAKKTLTLGGANIIGAGGGTIDLQANGG
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AGTNLGSATNPLAEINFGSKGVNVDTVLNVGEGVNL----YATNITTTDANVGSFVFNAG
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  (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Bacteriol. 170:3177-3188(1988).
-!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular characterization of the marcescens.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Outer membrane. SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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KVALQAAESTQTRKESKLSGNIDLGAGSSDSKE----
                                                                                                                                                                                                               NVNVKKDAIYQGTALNGGRGKTAVNAGGDIRLDQASDKQSESRSGFNVKASAKGGFTADS
                                                                                                                                                                                                                                                                    NDNVTDDEKKRAASV----KDVLNA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRASATVKTAVLATLLFATVQASANNETDLTSVGTEKLSFSANGNKVNITS-----
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                                                    --KDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKF
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Pred. No. 0.1
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W; D669B476FE7DAD51 CRC64;
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EMBL;
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EMBL;
                                                                        modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                       McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E. Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-ATCC 14028;
Stojiljkovic I., Valentine P., Heffron
"Salmonella typhimurium rhs homolog.";
Submitted (MAR-1999) to the EMBL/GenBan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella typhimurium.
Bacteria; Proteobacteria;
Enterobacteriaceae; Salmon
                                                                                                                                                                                                                                             cofactor."
                                                                                                                                                                                                                                                        Wu J.Y., Siegel L.M., Kredich N.M.; "High-level expression of Escherichia requirement for a cloned cysG plasmid
                                                                                                                                                                                                                                                                                                                          STRAIN-LT2;
                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-LT2 / SGSC1412 / ATCC 700720;
MEDLINE-21534948; PubMed-11677609;
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                                                                                                                                                                                            Bacteriol. 173:325-333(1991).
- CAUTION: Ref.3 sequence differs in positions 414 and 732.
                                                                                                                  s SWISS-PROT entry is copyright. It is produced through a cween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is
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   AF133696; AAD39458.1; -. AE008859; AAL22340.1; -. M64606; AAA27042.1; ALT_M64606; AAA27043.1; ALT_
                                                                                                                                                                                                                                                                                                                                                                 413:852-856(2001).
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                                                                                        DGEGTSIENKGDITSHGVYSVIRADNGSEVSNSGDILVYATSSNSSEDRAAITRASG
                                                                                                                     IGGGTYRGEAG-----YAI----GYSSISDGGNWIIKGTASGNSRGHFGASASVG
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 STANDARD; Q8X2C0;
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15 (INCOMPLETE).

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Gaps

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842 463 783

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MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoy.
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe (
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunay
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
DOMAIN
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[2]
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                                                                                                                                                                    Hypothetical
                                                                                                                                                                                                 PRINTS;
                                                                                                                                                                                                                                                                   EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-0157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli 0157:H7. Bacteria; Proteobacteria;
                                                                                                                                                                                                           Pfam;
                                                                                                                                                                                                                                                                                                          modified
                                                                                                                                                                                                                                                                                                                            the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21074935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterobacteriaceae;
                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                            InterPro; IPR003535;
                                                                                                                                                                                                                                        InterPro; IPR003344; Big_1.
                                                                                                                                                                                                                                                                                    rities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Contains 16 Big-1 domains.
SIMILARITY: BELONGS TO THE INTIMIN/INVASIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                            CAUTION:
                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                 CAUTION: Ref.2 sequence differs from that shown frameshift in position 1315.
                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produ
een the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                               AP002559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hetical protein
OR ECS2775/ECS
                                                                                                                                                                                                           PF02369; Big_1;
                                                                                                                                                                                                                                                                   AE005423;
                                                                                                                                                                              SM00634;
SM00089;
                                                                                                                                                                                                 PR01369;
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IPR000601; PKD_domain.
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35; PubMed=11206551;
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PKD; 8
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OBIG-1
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on update)
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Best Local
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P18127;
01-NOV-1990
01-NOV-1990
16-OCT-2001
Xanthomonas campestris pv. translucens.";
Mol. Gen. Genet. 223:163-166(1990).

-i- FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUC
-i- SUBCELLULAR LOCATION: Outer membrane (By similarity).

-i- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS
-CTAPESTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
                                                                                                                                                                                              Bacteria; Proteobacteria;
Xanthomonadaceae; Xanthomo
                                                                                                         Zhao J., Orser C.S.; "Conserved repetition in the ice nucleation
                                                                                                                                  MEDLINE=91080859; PubMed=2259339;
                                                                                                                                                 STRAIN-X56S;
                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                  NCBI_TaxID=343;
                                                                                                                                                                                                                          Xanthomonas
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Pred. No. 0.
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Matches 112
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Pfam; PF00818; Ice_nucleation; 81.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE_NUCLEATION; 57.
Ice_nucleation; Repeat; Outer_membran
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                                  --FGASASVGYQ 511
                                                                         QTAQESSSLTAGYGST--STAGYDSTLTAGYGSTQTAGYKSTLTAGYGSNSTAGHESSLI 1243
                                                                                                                                                --SNLTAGYGSTQTAREDSSLTAGYGSTSTAGHDSSLIAGYGSTQTAGYNSILTTGYGST 1185
                                                                                                                                                                                      RITHVAPGV-----KEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATA-GLV 452
                                                                                                                                                                                                                               LTAGYGST-QTARQGSDI-----TAGYGSTGT-AGADSSLIAGYGSTQTAGYD-----
                                                                                                                                                                                                                                                                                                          AGSD--SSLTAGY----GSTQTARQGSDVTAGYGSTGTAGADSTLIAGYGSTQTAGSDSS 1081
                                                                                                                                                                                                                                                                                                                                                 VSKDDQGNITYMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDET 340
                                                                                                                                                                                                                                                                                                                                                                                                                              STDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNYTFASGKGTTAT 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIAGYGSTQTSGSDSSLTAGYGSTQTARKGSDMTAGYGSTGTAGADSTLIAG-----YGS 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGS 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSTQTAGSDSSLTAGYGSTQTARKGSD------VTAGYGSTG----TAGADST 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSTLT----DTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVD 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAGADSTLIAGYGSTQTSGSDSSLTAGYGSTQTAREGSDVTAGYGSTGTAGADSTLISGY 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDVTAGYGSTGTAGADSTLIAGYGSTQTSGSDSSLTAGYGSTQ-TARKGSDITAGYGSTG 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SELTRNHTKRASATVKTAVLA------TLLFATVQASANNETDLT----SVG 61
                                                                                                             QAYLPGKSMMAIGGGTYRGEAGY----AIGYSSISDGG--NWIIKGTASGNSRGH-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TEKL-----SFSANGNKVNITSDTKGLNFAKE-----TAGTNGDTTVHLNGI 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1567 AA;
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Search completed: October 6, Job time: 11.9066 secs

2003, 09:23:55

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Result
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A;Molecule type: DNA
A;Residues: 1-591 <TET>
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A; Experimental source:
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ce: serogroup
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181.5 181	183 182 181.5	183 183	185 184	190 188	191.5 190.5	193.5 191.5
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adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B) (;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001 C;Accession: G81133 R.Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, ri, H.; Vanathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000 Science 287, 1809-1815, 2000 Science 287, 1809-1815, 2000 A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58 A; Reference number: A81000; MUID:20175755; PMID:10710307 A;Accession: G81133 SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF 161 YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120 TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV 281 TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV GB:AE002098; NID:g7226229; PIDN:AAF41395.1; PID:g722 B, strain MC58 0; Mismatches Score 2550.5; DB 2 Pred. No. 4.4e-125; ALIGNMENTS 0; ່ນ Indels Length 79; Gaps Rappuoli, R.; strain MC58. 300 221 240 54 60 Eisen,

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; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: A81888
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-592 <PAR>
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A;Experimental source: serogroup
C;Genetics:
A;Gene: NMA1200
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PVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPG
                                           TVNINAGNNIEISRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANK
                                                         TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSKKDNK
                                                                                                   TVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE
                                                                                                                   TVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE
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K.; Leather,
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Pred. No. 1.6e
L2; Mismatches
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S.; Moule, S.;
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Mungall,
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A; Molecule type: DNA
A; Residues: 1-2059 <SIN>
A; Cross references: GB.AE003982; GB:AE003849; NID:g9106554; PIDN:AAI
A; Experimental source: strain 9a5c
R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio,
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Cara
as Neto, E.; Docena, C.; E1-Dorry, H.; Facincani, A.P.; Ferreira, A.
submitted to GenBank, June 2000

NID:g9106554; PIDN:AAF84338.1;

GSPDB:GN

M.; Alvarenga, R.
raro, D.M.; Carrer

submitted to A; Authors: Fe

Ferreira,

Ferro,

J.A.;

Fraga,

J.S.;

Franca,

S.C.; Carraro,

Franco,

A;Title: The genome sequence of the plant pathogen Xylella A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number

number

below

A; Accession: D82671 A; Status: preliminary

C;Accession: D82671 R;anonymous, The Xylella fastidiosa Consortium of Nature 406, 151-157, 2000

the Organization

for

Nucleotide

fastidiosa A59328

surface protein XF1529 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000

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adhesin homolog H11732 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Oct-1997
C;Accession: 164138
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: 164138
A;Status: nucleic acid sequence not shown; translation not shown
A;Residues: 1-298 cTIGR>
A;Cross-references: GB:U32846; GB:L42023; NID:g1574588; PID:g1574589; TIGR:HI1732
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                                                                                   TGASTSVT-FSPSDIEKTRAATIKDVLNAGWNIKGAKVAGGNTENVDLVAGYDNVEFTTG
                                                                                                                       TGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSA 173
                                                                                                                                                                  VSDTLTIGGNTPAAGGATPKVSITSTADGLKLAK---GTNGDTAVHLNGLASTLPDVTTN
                                                                                                                                                                                                                                                STEDDIEDSAATKOONKNQALKAGOTLTLKAGKNLKAKLDQGGKSVTFALAKOLDVKTAK
                                                                                                                                                                                                                                                                                                                             MNKIFKVIWNVVTQTWVVVSELTRAHTKRTSATVATAVLATVLSATVQAINDAGTFVKVQ
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RESULT 5
A82615
Surface protein XF1981 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug
C;Accession: A82615
R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515, MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 bel A;Accession: A82615
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAMAIGTNAAVSGTESVALGK---NTNVSADNAVAI-GNG-----SVADRANSVSVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSTAIGRNAIASADGSVALGDGAKDGGRGAESYTGKYSGVQNNTVGTVSVGDAAKGETRS 1829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VKVSSNVLLDSNELVITSHSSTSSVKTLANGESVVNRTVVNGD---
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                                                                                                                                                                                                                                                                                                                                                                                                                       GNLRRETSGGVAAAIATANLPQAYVQGRGMTSVGVSSYQGQSAIAVGVSAVSESGHWVFK 2038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNAR----AGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIK 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGA 375
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                                                                                                                                                                                                                                                                                                                                                                          GTASGNSRGHFGASASVGYQW
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-12;
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1190 <SIM>
A;Residues: 1-1190 <SIM>
A;Cross references: GB:AE004017; GB:AE003849; NID:g9107083; PIDN:AAF84783.1; GSPDB:GN
A;Cross references: GB:AE004017; GB:AE003849; NID:g9107083; PIDN:AAF84783.1; GSPDB:GN
A;Cross references: GB:AE004017; GB:AE003849; NID:g9107083; PIDN:AAF84783.1; GSPDB:GN
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
as Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Jungueira, M.C., Mance, J.E.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Manck, C.F.M.; Miracca, E.C.; Miyaki, C.,
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
Rodriques, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
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                                                                                                                                                                                                                                                                      DALNVGSK----KDNKPV---------RITNVAPGVKEGDVTNVAQL 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTATVSKDDQGNITVMYDVNVGDALNVNQL----QNSGWNLDSKAVAGSSGKVISGNVS 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASGKGSTAIGRNAVASADGSVALGD-GAKDGARGAESYTGKYSGLQNNTVGTVSVGDASK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KSVHYYSTYD-----GGTQGGNYNGDGATGTRSIAVGVGTLASA----EGATAVGSGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GYTLGSMGLVITDGPSVTSSGI----NAGSQKITNVAAGTADTDAVNLSQLNTAMAGSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GESYDLKNTDGNIVISKESGSNDVLFNLSSSLKLDKLTVGDTVMTTNGV-----TVGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVVSELTRNHTKRASATVKTAVLATLLFATVQASANNETDLTSVGTEKLSFSAN-----
                                                                                                                                                                                                                                                                                                                                                                              PSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSV-----DG
                                                                                                                                                                                                                                                                                                                                                                                                                                 GETRTVS----NVADAKEAT--DAVNLRQLDRVAQDANRYVDNKIESLSEGQTF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENG-SSTDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATTNVTNDNVTDDEKKRAASVKDVLNAG-WNIKGVKPGTTASD---------
                                               IGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                        NQGLITAKQYTDGVVGSLRRDTDGGVAAAIATANLPQAYIPGRGMTSVGVSSYRGQSAIA 1154
                                                                                                                                                              KGVAQNLNNRIDNVDGNAR----AGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - NVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                            -SATP----IAAGVDATAIGVGATASGA
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AC0976
probable autotransporter sapB [imported] - Salmonella enterica subsp. C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov

18-Nov-2002

.; May Apoda

EDL93

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R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N. S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Ste A; Title: Complete genome sequence of a multiple drug resistant Salmonella enter A; Reference number: ABO502; MUID:21534947; PMID:11677608
A; Accession: AC0976
A; Status: preliminary A; Molecule type: DNA
A; Residues: 1-1107 < PARP>
A; Cross-references: GB:AL513382; PIDN:CAD03303.1; PID:g16504923; GSPDB:GN00176
C; Genetics:
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Best Local S
Matches 168
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   RGHFGASASVGYQW
                                        SGGIASAMAMAGLPQAYAPGANMTSIAGGTFNGESAVAIGVSMVSESGGWYYKLQGTSNS
                                                                       RAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNS
                                                                                                          LNLGDGSGGTTRIGNVSAAVNDTDAVNYAQLKRSVEEANTYTDQKMGEMNSKIKGIENKM
                                                                                                                                                                                ADEANTVSVGSSTQQR--RITNVAAGVNNTDAVNVAQLKASEAGSVRYETNADGSVNYSV
                                                                                                                                                                                                                 SVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLK-----
                                                                                                                                                                                                                                                      TRVTNIENGIGDIVTTGSTKYFKTNTDGADANAQGADSVAIGSGSIAAAENSVALGTNSV
                                                                                                                                                                                                                                                                                                                          GEFSVGSEDGQRQITNVAAGSADTDA---VNVGQLKVTDAQVSRNTQSITNLNTQVSNLD
                                                                                                                                                                                                                                                                                                                                                           ---AVAGSSGKVISGNVSPSKGKMDETVNINAG----NNIEITRNGKNI-----
                                                                                                                                                                                                                                                                                                                                                                                                GIGIGLNTLVMADAINGIAIGSNARANHANSIAMGNGSQTTRGAQTDYTAYNMDTPQNSV
                                                                                                                                                                                                                                                                                                                                                                                                                               G----QLQNSGWNLDSK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NVAAGALSEDSTDAVNGSQLYETNQKVDQNTSAIAD - - INT - SITNLGTDALSWDDEEGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDTKGLNFAKETAGTNG----DTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TDIAANTTNITQNSTAIENLNTSVSDINTSITGLTDNALLWDEDTGAFSANHGGSTSKIT
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                                                                                                                                                                                                                                                                                         ----DIATSMTPQF-----SSVSLGAGADAP----
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21.2%;
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Pred. No. 8.3e-12;
8; Mismatches 215;
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                                                                                                                                             ---GVAQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADKFETVTSGTNVTFASGKGTTA----TVSKDDQ
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1588 <STO>
A;Cross-references: GB:AE005174; NID:g12518349; PIDN:AAG58749.1; GSPDB:GN00145; UWGP:
                                    RESULT
H91188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: strain C; Genetics: A; Gene: Z5029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Genome sequence of enterohemorrhagic Escherichia A; Reference number: A85480; MUID:21074935; PMID:11206551 A; Accession: A86036
probable adhesin ECs448
C; Species: Escherichia
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Species: Escherichia coli
Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 150;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 KLSFSA----NGNK-----VNITSDTKGLNFAKETAGTNGDTTVHLNGI----GSTLTDT
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                                                                                                                                                                                AGIQW
                                                                                                                                             VGYQW
                                                                                                                                                                                                                 TAGLYQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASAS
                                                                                                                                                                                                                                                    --RISNVSAGVNNNDVVNYAQLKQSVQETKQYTDQRMVEMDNKLSKTESKLSGGIASAMA
                                                                                                                                                                                                                                                                                     PVRITNVAPGVKEGDVTNVAQLKGVAQ------NLNNRIDNVDGNARAGIAQAIA 447
                                                                                                                                                                                                                                                                                                                                                                                                                             KDDQGNIT-VMYDVNVGDALNVNQLQNS---GWNLDSKAVAGSSGKVISGNVSPSKGKMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSTKYFKTNTDGVDA--SAQGKDSVAIGSGSIAAAD--NSVALGTG-SVATEENTISVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSADTDAVNVG-----QLKVTDAQVSQNTQSITNLDNR-VTNLDSRVTNIENGIGDIVTT 1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKG----ENG----SST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEF
                                                                                                                                                                                                                                                                                                                                                         ETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNK 398
                                                                                                                                                                                                                                                                                                                                                                                                STNQRRITNVAAGKNATDAVNVAQLKSSEAGGVRYDTKA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVS
                    ECs4480
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                                                                                                              1588
   coli
                    [similarity] -
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27.5%;
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K.; A
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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Nov-2001 C;Accession: H91188
C;Accession: H91188
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; H gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: H91188
                                                    probable surface protein (partial) YPO0902 [imported] - Yersinia pestis (strain CO92 C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AH-0110
C;Accession: AH-0110
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Toonin, A.; Davies, R.M.; Davis, P.; Dougan, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, deno-Tarraga, A.M.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre
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A;Nolecule type: DNA
A;Residues: 1-1588 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB37903.1; PID:g13363955;
A;Cross-references: strain O157:H7, substrain RIMD 0509952
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A; Title: Genome sequence of Yersinia pestis, the causative agent A; Reference number: AB0001; MUID:21470413; PMID:11586360
                                        deno-Tarraga, A.M.; Chillingworth, T.; Cronin,
il, M.; Rutherford, K.; Simmonds, M.; Skelton,
Nature 413, 523-527, 2001
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-658 <KUR>
A; Cross references: GB:A'
C; GenetLcs:
A; Gene: YP00902
A; Molecule type: DNA
A; Residues: 1-1091 <BLAT>
A; Cross-references: GB: AE000291;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQN----LNNRIDNVDGNAR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNSSGLAKPSATGANSATGGAGSVASGNNSTAFGSGAKATAANSAALGANSVADRANSVS
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                                                                                                 e sequence of Escherichia coli
MUID:97426617; PMID:9278503
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                                                            not
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  GB:U00096; NID:g1788298; PIDN:AAC75061.1; PID:g17883
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                                                            shown;
                                                                                                                                                                            Bloch, C.A.; Perna, N.T.;
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332 189 272

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467 343 424

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A;Molecule type: DNA
A;Residues: 1-1004 (SIM>
A;Residues: 1-1004 (SIM>
A;Residues: 1-1004 (SIM>
A;Cross-references: GB:AE003981; GB:AE003849; NID:g9106543; PIDN:AAF84325.1; A;Cross-references: Strain 9a5c
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvar Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, I.E.A.; Carraro, D.M. as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.;
                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11

CR3672

Surface-exposed outer membrane protein
CrSpecies: Xylella fastidiosa
CrDate: 18-Aug-2000 #sequence_revision
CrAccession: CR3672
CrAccession: CR3672
                                                                                                                                                                                                                                          A;Title: The genome sequence of the plant pathogen Xylella A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A;Accession: C82672 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                R;anonymous, The Ar-
mature 406, 151-157, 2000
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Pred. No. 2.9e-05;
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                 S.C.; Franco, M.C.; Frohm J.E.; Kuramae, E.E.; Laign Marques, M.V.; Martins, H
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RESULT 12
\$28634
adhesin AIDA-I precursor - Escherichia
C:Species: Escherichia coli
C:Date: 17-Apr-1993 #sequence\_revision
C:Accession: \$28634; \$22680; \$28881; \$7
R:Benz, I.

submitted to the EMBL Data A; Reference number: \$28634 A; Accession: \$28634

Library, March

on 17-Apr-1993 S72657

#text\_change

08-Oct-1999

coli plasmid

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAVLAT - - - LLFATVQASANNETDL - - TSVGTEKLS - - - - - -
DGSVSLGFNSFVRQSGEHGVALGTDAGVSGKDSIALGY
                                                                                                                      TGPAVR----RIVNVGDGIGNNDAVNKSQLDGVTASVNDVAASVKKIVGTIQITGSGVA
                                                                                                                                                                                                                                                                                                                                             ΕVΙ
                                                                                                                                                                                                                                                                                                                                                                                                                                       KESTAIGSGAQAVADNTVAFGGRAIANAVGASALGFDSHAKGINSTTVGTQSVSLGQGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPAVRRIVNVGDGIGNNDAVN-KSQLDGVTASVN-DVAASVKTIALTNQVTGSSVASASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NKIYRIIWNSALNAWVVVSELT------RNH-----RNH-----
                             YSSISDGGNWIIK-----GTASGNSRGHFGA-SASVGY
                                                          SAIGKDSTATGASAQAVGDSSVALGTRATANAIGSSVLGVDSRARGINSTALGRQSNAIG
                                                                                       QAI---ATAGLVQAYLPGKSMMAIG-----
                                                                                                                                                     NVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNN---RIDNVDGNAR---AGIA
                                                                                                                                                                                      ---YNSFVGQSATNGIALGSN-----AIVSGVNSVALGAGSVASELNVISVGGGDGV
                                                                                                                                                                                                                   KGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSV----DGDAL
                                                                                                                                                                                                                                                                               VSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLD-----SKAVAGSSGKVISGNVSPS
                                                                                                                                                                                                                                                                                                              RIVNVGDGIGNNDAVNKSQLDGVTASVNDVVASVKNIAGAIQITGSGVASVSGQDSTAAG
                                                                                                                                                                                                                                                                                                                                                                          SLGYNSFYGEGSFNGLALGSNSLYLLQGYDSYALGSGSMASEPNYVSVGSGDGLRGPAVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDEKKRAASVKDVL - - NAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAPNAIALGYN-SSVTQSANNGVALGSNSTVSGVNSVALGAGSMASELNVISVGGGDGVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPAMVTASKVMVAHVDSQVNRTADRIPTGDGSELMTHMALDWKFFPFGNNSIAIGYFSKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NQIYRKFWNLSLGSWSVASHMTNDGGCSDVVLRHSGVRNRSLVLAIGLALTSVTHAQSVK
                                                                                                                                                                                                                                                  ASAQAAGDSSIA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·GLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTNVTN------DNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.0%;
21.6%;
                                                                                                                                                                                                                                                                                                                                          -DAVNKAGWRMKTTTANGQTGQADKFETV--TSGTNVTFASGKGTTAT-
                                                                                                                                                                                                                                                  - LGARSRANAIGSSALGVDGHALGANSTALGGQSTAISEGGTSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86;
                                                                                                                                                                                                                                                                                                                                                                                                        ----KLVTGKDKGENGS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 234;
Pred. No. 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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.8e-05;
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678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -FSANGNKVNITSDTK-
                                                                                                                                                                                                                                                                                                                                                                                                        -STDEGEGL -- VTAK
                                                                                       -GGTYRGEAGYAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -TKRASATVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVIKEKDG-
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Palmieri,
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Silv
A.L.
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C;Keywords: membrane protein
F;1-49/Domain: signal sequence #status predicted <SIG>
F;50-1286/Product: adhesin AIDA-I #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-1286 <BEN>
A;Residues: 1-1286 <BEN>
A;COSS-references: EMBL:X65022; NID:g42254; PIDN:CAA46156.1; PID:g42255
A;COSS-references: EMBL:X65022; NID:g42254; PIDN:CAA46156.1; PID:g42255
R;Benz, I.; Schmidt, M.A.
Mol. Microbiol. 6, 1539-1546, 1992
Mol. Microbiol. 6, 1539-1546, 1992
A;Title: AIDA-I, the adhesin involved in diffuse adherence of the diarrhoeagenic Esca;Reference number: S22680; MUID:92326638; PMID:1625582
A;Accession: S22680
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R;Suhr, M.; Benz, I.; Schmidt, M.A.
Mol. Microbiol. 22, 31-42, 1996
A;Title: Processing of the AIDA-I precursor: removal of AIDA and evidence for the A;Reference number: S72657; MUID:97055419; PMID:8899706
A;Accession: S72657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 839-1286 <BE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: DAEC strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein A; Residues: 847-856 <SUH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein A; Residues: 50-56 <BE3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S28881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X65022
A;Experimental source: strain 2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                       417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 SADTKTTTVN-----VESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGEN-----GS 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 LNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 LTSVGTEKLSFSANGNKVNITSDTKGL----NFAKETAGT-NGDTTVHLNGIGSTLTDTL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TVSSGETQIVYSGRGNS-NATVNSGGTQIVNNGGKTTATTVNSSGSQNVGTSGATIS-TI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MNKIYRIIWNSALNAWVVVSELTRNH--TKRASATVKTAVLATL--LFATVQASANNETD
                   VA-QLKGVAQNLNNRIDNVDGN----
                                                                                                                                                                                                                                                                                                                                 NVTFASGKGTTATVSKD-----DQGNITVMYDVNV------GDALNVN-----QLQNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MNKAYSIIWSHSRQAWIVASELARGHGFVLAKNTLLVLAVVSTIGNAFAVNISGTVSSGG
                                                                                                                                                                                                                                                                                                              QTVFAGATVTDTTVNSGGNQNISSGGIVSETTVNVSGTQNIYSGGSALSANIKGSQIVNS
                                                                                                                                                                                                                                                                                                                                                                                               NATE ---
                                                                                                                                                                                                                                                                                                                                                                                                                                  STDEGEGLYTAKEVIDAVNKAGWRMKT-----TTANGQT-----GQADKFETVTSGT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGITDSTNISSGGQQRVSSGGVASNTTINSSGAQNILSE-EGAISTHISSGGNQYISAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VNSGGIQRVSSGGV-----ASATNLSGGAQNIYNL---GHASNTVIFSGGNQTI-FS 166
                                                            PVQNSVVVTRTVSSAAKPFDAEVYSGGKQTVYLWRGIWYSNFLTAVWSMFPGTASGANVN
                                                                                                                                         ARGTILNNSGRENVSNGGVSYNAMINTGGNQYIYSDGEATAAIVNTSGFQRIN--SGGTA
                                                                                                                                                                                      -----KNID----
                                                                                                                                                                                                                          EGTAINTLYSDGGYQHIRNGGIASGTIVNQSGYVNISSGGYAESTIINSGGTLRVLSDGY
                                                                                                                                                                                                                                                                   -GWNLDSKAVAG------SSGKVI--SGNVSPSKGKMDETVNINAGNNIEITRNG-
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                                                                                                                                                                                                                                                                                                                                                                                           ---TIVNSGGFQRVNSGAVATGTVLSGGTQNVSSGGSAISTSVYNSGV 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 222; DB 2;
; Pred. No. 0.00056;
88; Mismatches 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2787
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                                                                                                                                                                                 ----IATSMTPQFSSVSLGAGADA
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                                                                                                    -DNKPVRITNVAPGVKEGDVTN
                     -----ARAGIA 443
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330 NVTDKGHWNFLGTGEAFRYIYIGDAGDGELNVSSEGKVDSGIITAG----MKETGTGNITV 386
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CTNIKNGGTIRVDSGASALNIALSSGGN 487		Db	513 LSGRLNAFAGNVVGTILNQEGRQYVYSGATATSTVGNNEGREYVLSGGITDGTVLNSGGL 572
RESULT 13 AVSSEGRASATVINEGGACFYDGGQYTGTHIKNGTIKNGSTANALALIALSSGUN 629 RESULT 13 Aydes protein		Qy	QAIATAGLVQAYLPGKSMMAIGGTYRGEAGYAIGYSSISDGGN
RESULT 13  RESULT 13  RESULT 13  RESULT 13  RESULT 14  RESULT 14  RESULT 15	cheri	Db	QAVSSGGKASATVINEGGAQFVYDGQVTGTNIKNGGTIRVDSGASALNIALSSGGN
Righteriate names: Protein Colored Republication (C. Species Escherichia coli C: Species Escherichia coli C: Species Escherichia coli C: Checasion: Ad4005, 152440, 53415 C: Checasion: Ad4005, 152440, 534315 R. Ribattner, F. R.: Plunkett III, G.; Bloch, C.A.; Berna, N.T.; Burland, V.; Riley, M. A.: Rose, D. J.; Mau, B. Shao, Y. Science 277, 1433-1463, 1997 R. Ribattner, F. R.: Plunkett III, G.; Bloch, C.A.; Berna, N.T.; Burland, V.; Riley, M. R.: Nose, D. J.; Mau, B. Shao, Y. R. Ribattner, F. R.: Plunkett III, G.; Bloch, C.A.; Berna, N.T.; Burland, V.; Riley, M. R.: Nose, D. J.; Mau, B. Shao, Y. R. Ribattner, F. R.: Plunkett III, G.; Bloch, C.A.; Berna, N.T.; Burland, V.; Riley, M. R.: Nose; D. J.; Mau, B.; Shao, Y. R. Ribattner, F. R.: Plunkett III, G.; Bloch, C.A.; Berna, N.T.; Burland, N. Ribits, M.; Lithgav, T.; Bol, P.; Boogenraad, N. R.: Science 277, 1433-1465, 1997 R. Rocartwright, P.; Timms, M.; Lithgav, T.; Bol, P.; Boogenraad, N. R.: Rocartwright, P.; Timms, M.; Lithgav, T.; Bol, P.; Boogenraad, N. R.: Rocartwright, P.; Timms, M.; Lithgav, T.; Bol, P.; Boogenraad, N. R.: Rocartwright, P.; Timms, M.; Lithgav, T.; Bol, P.; Boogenraad, N. R.: Rocartwright, P.; Timms, M.; Lithgav, T.; Bol, P.; Boogenraad, N. R.: Rocartwright, P.; Timms, M.; Lithgav, T.; Bol, P.; Boogenraad, N. R.: Rocartwright, P.; Timms, M.; Lithgav, T.; Bol, P.; Boogenraad, N. R.: Rocartwright, P.; Timms, M.; Lithgav, T.; Bol, P.; Boogenraad, N. R.: Rocartwright, P.; Timms, M.; Lithgav, T.; Bol, P.; Boogenraad, N. R.: Rocartwright, R.; Rocartw			- Fecherichia coli cetrain K-1
A.; Rose, D.J.; Mau, B.; Shao, Y.  Science 277, 1433-1462, 1997  A.Fitle: The complete genome sequence of Escherichia coli K-12.  A.Fitle: The complete genome sequence of Escherichia coli K-12.  A.Fitle: The complete genome sequence of Escherichia coli K-12.  A.Fitle: The complete genome sequence of Escherichia coli K-12.  A.Fitle: The complete genome sequence of Escherichia coli K-12.  A.Fitle: The complete genome sequence of Escherichia coli K-12.  A.Fitle: A.Fitle		N; Alterna C; Species C; Date: 1 C; Accessi R; Blattne	<pre>station 17-Sep-1997 #text_change 01-Mar-2002 s34315 II, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley,</pre>
Kolecule type: DNA Residues: 1.1325 CALATY Cross-references: GB-ABODO248; GB:U00096; NID:91787783; PIDN:AAC74583.1; PID:91787 Experimental source: Strain K-12, substrain Mc1655 Cartwright, P; Timms, M; Lithgow, T; Ho), P; Hoogenraad, N. Corhum. Blophys. Acta 1153, 345-447, 1993 Cross-references: CB-ABODO248; GB:U00096; NID:9178755 Status: translated from GB/EMEL/DDBJ Kolecule type: DNA, K', 885-1316, 'S',1318-1325 CRESS Cross-references: EMBL:X7395; NID:9312392; PIDN:CAA51730.1; PID:9312393 Kole: the difference in length is due to a frameshift error at pos 653 Genetics: Genetics: Genetics: Genetics: Genetics: MREL:X7395; NID:9312392; PIDN:CAA51730.1; PID:9312393 Kole: the difference in length is due to a frameshift error at pos 653 Genetics: Genetics: Genetics: Genetics: MREL:X7395; NID:9312392; PIDN:CAA51730.1; PID:9312393 TOT-19/Region: nucleotide binding; P-loop T12-719/Region: nucleotide binding; P-loop T12-719/Region: nucleotide binding; P-loop T12-719/Region: nucleotide binding; P-loop T13-719/Region: nucleotide binding; P-loop T14-111; T11; T11; T11; T11; T11; T11; T125; MRETCHARLANGAVIVVEELTR	uter	A; Referen A; Accessi	so, Y. sequence of Escherichia coli K-12. sUID:97426617; PMID:9278503
Experimental source: GH.ABUUUV48; GH:UUUV95; NLD;GLN8/SB; PLIN;AAC/4583.1; PLID;LAB, Experimental source: Strain K-125. substrain M61652 cochim. Biophys. Acta 113; 345-347, 1993 entitle: An Escherichia coli gene showing a potential ancestral relationship to the Reference number: 152440; MUID:94100243; PMID:8274505 Accession. 152440; Mulding: PLOOP Accession. 152440; Mulding: PLOOP Accession. 152440; Mulding: PLOOP Accession. 152440; Mulding: Proop Accession. 152440; Mulding: Pro		A; Status: A; Molecul A; Residue	not shown; translation not shown
TRILE: An Exchange in Coli gene Showing a potential ancestral relationship to the Reference number: 152400; MUID:94100243; PMID:8274505 Accession: 152400 Status: translated from GB/EMBL/DDBJ Molecule type: DNA Residues: 689-883, 'K', 985-1316, 'S', 1318-1325 <res> Cross-references: DMELT/3295; NID:9312392; PIDN:CAA51730.1; PID:9312393 Rote: the difference in length is due to a frameshift error at pos 653 Genetics: Genetics: Genetics: Genetics: Description: probably involved in protein translocation apparatus Reywords: nucleotide binding; P-loop 712-719/Region: nucleotide-binding motif A (P-loop) 712-719/Region: nucleotide-binding motif A (P-loop) Rest Local Similarity 24.5%; Pred. No. 0.0014; 1 MNRIYRIIMNGALOWFOACSELTRNHTKRASATVKTAVLATLLFATVOAS 50 1</res>			GB:000096; NID:91/8//83; PIDN:AAC/4583.1; 12, substrain MG1655 hgow, T.; Hoj, P.; Hoogenraad, N.
Molecule type: DNA  Rosidues: 689-883, 'K', 885-1316, 'S', 1318-1325 <res> Residues: 689-883, 'K', 885-1316, 'S', 1318-1325 <res> Cross-references: EMBL:X73295; NID:g312392; PIDN:CAA51730.1; PID:g312393 Rote: the difference in length is due to a frameshift error at pos 653 Residues: 689-883, 'K', 885-1316, 'S', 1318-1325 <res> Cross-references: EMBL:X73295; NID:g312392; PIDN:CAA51730.1; PID:g312393 Rote: the difference in length is due to a frameshift error at pos 653 Rote: the difference in length is due to a frameshift error at pos 653 Rote: the difference in length is due to a frameshift error at pos 653 Rote: the difference in length is due to a frameshift error at pos 653 Rote: the difference in length is due to a frameshift error at pos 653 Rote: the difference in length is due to a frameshift error at pos 653 Rote: the difference in length is due to a frameshift error at pos 653 Rote: the difference in length is due to a frameshift error at pos 653 Rote: the difference in length is due to a frameshift error at pos 653 Rote: The difference in length is 25; Indels 137; Gaps Rote: The difference in length is 25; Indels 137; Gaps Rote: The difference in length is 250; Indels 137; Gaps Rote: The difference in length is 250; Indels 137; Gaps Rote: The difference in length is 250; Indels 137; Gaps Rote: The difference in length is 250; Indels 137; Gaps Rote: The difference in length is 250; Indels 137; Gaps Rote: The difference in length is 250; Indels 137; Gaps Rote: The difference in length is 250; Indels 137; Gaps Rote: The difference in length is 250; Indels 137; Gaps Rote: The difference in length is 250; Indels 137; Gaps Rote: The difference in length is 250; Indels 137; Gaps Rote: The difference in length is 250; Indels 137; Gaps Rote: The difference in length in lengt</res></res></res>		A; Title: A; Referen A; Accessi	chia coli gene showing a potential ancestral relationship to IS2440; MUID:94100243; PMID:8274505
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Reywords: nucleotide binding; p-loop 712-719/Region: nucleotide binding; p-loop 712-719/Region: nucleotide-binding motif A (P-loop)  Query Match			resobable intellect in protects two polices of the protect of the
Query Match  8.2%; Score 214.5; DB 2; Length 1325;  Best Local Similarity 24.5%; Pred: No. 0.0014;  Matches 146; Conservative 62; Mismatches 250; Indels 137; Gaps  1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQAS 5  1 MNRIYRVIWNCTLQVFQACSELTRRAGKTSTVNLRKSGLTTKESRLTLGVLLALSGSAS 6  MNRIYRVIWNCTLQVFQACSELTRRAGKTSTVNLRKSGLTTKFSRLTLGVLLALSGSAS 6  1 SUMMIT REVIEW COLOR 1 STANGAR STATE 1 STANGAR ST		;712-	otide-binding motif A (P-
1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQAS     :     :     :       :		Ž 1~	atch 8.2%; Score 214.5; DB 2; Length 1325; cal Similarity 24.5%; Pred. No. 0.0014; 146; Conservative 62; Mismatches 250; Indels 137; Gaps
1 MNRIYRVIWNCTLQVFQACSELTRRAGKTSTVNLRKSSGLTTKFSRLTLGVLLALSGSAS  51ANNETDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGT		Qy	MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQAS
11 GASLEVDNDQITNIDTDVAYDAYLVGWYGTGVLNILAGGN-ASLTTITTSVIGA  93 NGDTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLN  114 NEDSEGTVNLLGGTWRLYDSGNNARPLNVGQSGTGTLNIKQKGHVDGGYLR  114 NEDSEGTVNVLGGTWRLYDSGNNARPLNVGQSGTGTLNIKQKGHVDG		<u>ַ</u>	MNRII KVIWNCIUQVEQACSELI KRAGAISTVNLKASSSGLI TRESKLITUSVLLALSGSAS
93 NGDTTVHLNGIGSTLIDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLN		db 43	GASLEVDNDQITNIDTDVAYDAYLVGWYGTGVLNILAGGN-ASLTTITTSVIGA
114 NEDSEGTVNVLGGTWRLYDSGNNARPLNVGQSGTGTLNIKQKGHVDGGYLR  142 AGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVK  143 AGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVK  144 AGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTE		Qy	NGDTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLN
142 AGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVK		Db	NEDSEGTVNVLGGTWRLYDSGNNARPLNVGQSGTGTLNIKQKGHVDGGYLR
165 LGSSTGGVGTVNVEGEDSYLTTELFEIGSYGTGSLNITDKGYVTSSIVAILGYQ  195 IGAKTSVIKEKDGK-LVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRM		Qy	AGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVK
195 IGAKTSVIKEKDGK-LVTGKDKG			POSSESSE CARRAGORDALTATION PROPERTY DIVINITY DIV
246 KTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDALNV		Qy Db	IGAKTSVIKEKDGK-LYTGKDKGENGSSTDEGEGLYTAKEVIDAVNKAGWRM  :  :
276 -IGTLNVQDQDSVITVRRLYNGYEGNGTVNISNNGLINNKEYSLVGVQDGSHGVV 304 NQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDET		Qy	KTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDALNV
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A; Experimental source: C; Genetics:
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AldA-I adhesin-like protein [imported] - Escherichia coli (strain 0157:H7, C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: D90803
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: D90803
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A;Experimental source: strain 0157:H7, substrain RIMD 0509952
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A; Residues: 1-949 <HAY>
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    GHRGTLTLAAGGSLSGRTQLSKGASMVLNGDVVSTGDIVNAGEI---
                                                                                                                       NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSKKDNKPV
                                                                                                                                                               NRLGNFT----VENGKADGV--VLESGGRLDVLESHSAQNTLVDDGGTLAVSAGGKATSV
                                                                                                                                                                                                       DQ-GNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVI--SGNVSPSKGKMDETV
                                                                                                                                                                                                                                               NEGGWQVVKAGGAAGNTTINQNGELRVHAGGEATAVTQNTGGALVT----STAATVIGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----IGSTLTDTLLNTG-----
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                                                                                 TITSGGAL-IADSGATVE-GTNASGKFSIDGTSGQASGLLLENGGSFTVNAGGQAGNTTV
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                                            ---RITNVAPG--
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21.9%; Pred. No. 0.001;
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Shiba, T.; Hattori, M.; Shinagawa,
                                         -VKEGDVTNVAQLKGVAQNLNNRIDNVDG
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C;Accession: H85611; B85663
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A;Residues: 1-1005 <ST2>
A;Cross-references: GB:AE005174; NID:gl2514546; PIDN:AAG55766.1;
A;Experimental source: strain O157:H7, substrain EDL933
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C; Species: Escherichia coli
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                                                                               NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSKKDNKPV
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Pred. No. 0.0011;
/9; Mismatches 213;
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Result
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Maximum DB
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A surface protein
N. meningitidis H4
N. meningitidis Z2
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A surface protein
N. meningitidis H1
N. meningitidis H1
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Moraxella catarrha Moraxella catarrha	su	inf		emophilus	O		influ	Haemophilus adhesi	S		Haemophilus influe	influ	Ð	N. meningitidis PM	N. meningitidis PM	N. meningitidis su	N. meningitidis PM	N. meningitidis PM	N. meningitidis P2	A surface protein	A surface protein	itidis	A surface protein	N. meningitidis PM	face p	cid se	O	N. meningitidis H4	ngitidis	mino a	A surface protein	itidis	A surface protein	N. meningitidis BZ

## ALIGNMENTS

Surface protein; surface glycoprotein; infection; vaccine; immunoreactive peptide. N-PSDB; AAX85796 WPI; 1999-418754/35 Jennings MP, VIND ( DOAD) 14-DEC-1998; 24-JUN-1999 Neisseria meningitidis. A surface protein of Neisseria meningitidis 08-SEP-1999 AAY23744; AAY23744 standard; Protein; 12-DEC-1997; WO9931132-A1 INNOVATION LTD. QUEENSLAND. (first entry) Moxon 97GB-0026398 98WO-AU01031 Peak 592 ₽

Neisseria meningitidis surface proteins useful for treating

Neisseria meningitidis strain H41.

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RESULT 2
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Best Local S
Matches 541
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             Surface antigen NhhA;
                                                               24-OCT-2001
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                                                                                                                standard;
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           meningococcal disease; meningitis vaccine
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237..592
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New NhhA surface antigen polypeptides and polynucleotides Neisseria meningitidis, useful in producing vaccines for the preventing broad spectrum of Neisseria meningitidis treating õ

Claim 9; Fig 1; 91pp; English

The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhha (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectivel immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen Nhha from N. meningitidis strain H41 is 1 of 10 Nhha polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given i present invention ing of effectively

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                                                                                                                                          antigen NhhA; meningococcal disease; meningitis vaccine
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115..124
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/note= "Variable
103..114
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Pred. No. 1.2e-150;
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                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                            New NhhA surface antigen polypeptides and polynucleotides Neisseria meningitidis, useful in producing vaccines for preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                            Claim
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DB; AASO9170.
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TTA--SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLV
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/note= "Variable
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/note= "Variable
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189..208
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Pred. No. 1.3e-138;
9; Mismatches 23;
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14-JAN-1998;
01-SEP-1998;
                  meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167) encoding the proteins. Compositions comprising the protein, nucleic acid or antibody specific to the protein are useful as pharmaceuticals, e.g. vaccine composition or a diagnostic composition. The composition is also useful for treating or preventing an infection due to Neisserial
                                                                                        Claim
                                                                                                          diagnostic compositions meningitidis infections
                                                                                                                   New protein and its nucleotide sequence, diagnostic compositions for treating and,
                                                                    The invention provides proteins (AAY27201-245) from Neisseria
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DB; AAX99125.
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          especially
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98GB-0000760.
98GB-0019015.
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          meningitidis.
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RESULT 5
AAX23743
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XX AAX23743
AC AAX2
XX BUF O8-S
DT 08-S
DT 08-S
XX SULF
KW Inmnu
XX Sulf
KW Inmnu
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XX Neis
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PF 14-D
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Best Local
                                                                                                                                                                                A surface protein of Neisseria meningitidis
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                                         12-DEC-1997;
                                                              14-DEC-1998;
                                                                                    24 - JUN - 1999
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24-OCT-2001

(first entry)

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RESULT 6
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Matches 496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especial in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
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                           AAU06176
                                                                           AAU06176 standard;
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Pred. No. 5.5e-134;
1; Mismatches 33; I
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N. meningitidis
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhha (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding whild-type surface antigen. The present sequence representing the wild type surface antigen Nhha from N. meningitidis strain H38 is 1 of 10 Nhha polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                   New NhhA surface antigen polypeptides and polynucleotides Neisseria meningitidis, useful in producing vaccines for t preventing broad spectrum of Neisseria meningitidis -
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The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kba. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
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                                                                                                                           VIKEKDGKLYTGKGKGENGSSTDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKF
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                                                                                                                                                                                                         SSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAP
                                                                AGIAQAIATAGLAQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSR
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                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                 VIKEKDGKLVTGKGKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKF
                                                                                                                               NAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTS
                                                                                                                                                                                                                                                                               EDEEEELESVQR-SVVGSIQASMEGSVELETISLSMTNDSKEFVDPYI-----VVT
           SSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAP
                                                      ETVTSGTKVTFASGNGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAG
                                                                                                                                                                           KGLNFAKETAGTNGDTTVHLNGIGSTLTDMLLNTGATTNVTNDNVTDDEKKRAASVKDVL
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                                                                                      VIKEKDGKLYTGKGKDENGSSTDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKF
SSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAP
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89.2%;
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New NhhA surface antigen polypeptides and polynucleotides from

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Best Local Sin
Matches 493;
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                AAU06178;
                                                AAU06178 standard;
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diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain BZ10 is 1 of 10 NhhA polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                            New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treat preventing broad spectrum of Neisseria meningitidis -
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                                                                                                                                                                    meningitidis mutant polypeptides of the surface antigen NhhA (AAUU6182-AAUU6186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particular the deletion of variable regions. The deletion mutants are useful
                                                                                                                                                                                                                                                                                                        Claim
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51..104
/label= V1
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236. 242
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/note= "Conserved
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         (UYQU)
                                                                                                                                           Surface
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                                                                                             W09931132-A1
                                                                                                                                  Surface protein; immunoreactive p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                      12-DEC-1997;
                                                        14-DEC-1998;
                                                                           24-JUN-1999
                                                                                                              Neisseria meningitidis
                                                                                                                                                               surface
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                                                                                                                                                                                                                                                                                                                                            VIKEKDGKLYTGKGKGENGSSTDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKF
                                                                                                                                                                                                                                                                             GHFGASASVGYQW
                                                                                                                                                                                                                                                                                                                   AGIAQAIATAGLVQAYLPGKSMMAIGGGTYLGEAGYAIGYSSISAGGNWIIKGTASGNSR
                                                                                                                                                                                                                                                                                                                                                                                 NAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KGLNFAKETAGTINGDTTVHLNGIGSTLTDMLLNTGATTNVTNDNVTDDEKKRAASVKDVL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKAGDNLKIKONTNENTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKAGDNLKIKQNTNENTNA----SSFTYSLKKDLTGLINVETEKLSFGANGKKVNIISDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDEEEELESVQR-SVVGSIQASMEGSVELETISLSMTNDSKEFVDPYI------VVT
                                                                                                                                                                                                                      standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDDDLYLEPVQRTAVVLSFRSDKEGTGEKEG----TEDSNWAV--YFDEKRVLKAGAIT 105
                                                                                                                                                                                                                                                                     GHFGTSASVGYQW
                                                                                                                                                                                                                                                                                                        AGIAQAIATAGLAQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSR
                                                                                                                                                             protein of Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               598
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        INNOVATION LTD QUEENSLAND.
                                                                                                                                                                                (first entry)
                                                                                                                                 n; surface
peptide.
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                                      97GB-0026398
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                                                                                                                                           glycoprotein; infection;
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                                                                                                                                                                                                                      594
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Pred. No. 9.1e-133;
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RESULT 12
AAU06179
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AC AAU06
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Best Local Simi
Matches 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kba. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    meningitidis
                            AAU06179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1999-418754/35.
DB; AAX85791.
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                                                                                                                                                                                        LKAGDNLKIKQNTNENTNASSFTYSLKKDLTGLINVETEKLSFGANGKKVNIISDTKGLN 112
                                                                                                                                                                                                                                                                                                                                                                                                                       DDEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVNGNARAGIA 472
                                                                                                                                                                                                                                                                                                                                                                                                                                 EDEEEELESVQR-SVVGSIQASMEGSVELETISLSMTNDSKEFVDPYI------VVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 95-97; 132pp; English.
                                                                                    ASASVGYQW
                                                                                                                                                                                                                                       SGTKVTFASGNGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGK 352
                                                                                                                                                                                                                                                                    KDGKLVTGKGKDENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVT
                                                                                                                                                                                                                                                                            KDGKLVTGKGKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVT 292
                                                                                                                                                                                                                                                                                                         NIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKE
                                                                                                                                                                                                                                                                                                                   NIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKE
                            standard;
                                                                          ASASVGYQW
                                                                                                                                                                                                                               SGTNVTFASGKGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 594 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Moxon
                           Protein;
                                                                                           541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             surface proteins useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 2423.5; DB 2
Pred. No. 1.3e-132;
0; Mismatches 31;
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhhA (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than
                                                                                                                                                                                                                                                                                                           Claim
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Region
                 would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain BZ198 is 1 of 10 NhhA polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                               New NhhA surface antigen polypeptides and polynucleotides Neisseria meningitidis, useful in producing vaccines for t preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-488774/53.
N-PSDB; AAS09169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JAN-2001; 2001WO-AU00069
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present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigen NhhA; meningococcal disease; meningitis vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               meningitidis strain BZ198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jennings
    invention.
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/note= "Variable
239..594
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232..23
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213..231
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191..212
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105..116
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127..190
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XX O8-SE
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COS Neiss
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                                                                                                                                       Surface protein; immunoreactive pe
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         (UYQU ) UNIV
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                                                                                                                                                                                                                               AAY23740 standard;
                                       12-DEC-1997;
                                                           14-DEC-1998;
                                                                              24-JUN-1999
                                                                                                  WO9931132-A1
                                                                                                                     Neisseria meningitidis
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                                                                                                                                                                                                                                                                                                                                                                                                             VISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSV
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                                                                                                                                                                                                                                                                                                                                QAIATAGLVQAYLPGKSMMAIGGGTYLGEAGYAIGYSSISAGGNWIIKGTASGNSRGHFG
                                                                                                                                                                                                                                                                                                                                                                      DDEGALNYGSKDANKPYRITNYAPGYKEGDYTNYAQLKGYAQNLNNRIDNYNGNARAGIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KDGKLYTGKGKGENGSSTDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DDDDLYLEPVQRTAVVLSFRSDKEGTGEKEG-----TEDSNWAV--YFDEKRVLKAGAIT
                                                                                                                                                                                                                                                                                                   ASASVGYQW
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                                                                                                                                                                                                                                                                                                                     QAIATAGLVQAYLPGKSMMAIGGDTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFG
                                                                                                                                                                                                                                                                                                                                                             DDEGALNVGSKDTNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIA
                                                                                                                                                                                                                                                                                                                                                                                                   VISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSV
                                                                                                                                                                                                                                                                                                                                                                                                                                          SGTNVTFASGKGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGK
                                                                                                                                                                    protein of Neisseria meningitidis
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         INNOVATION LTD QUEENSLAND.
                                                                                                                                       n; surface
peptide.
                                        97GB-0026398
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Pred. No. 1.3
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RESULT 14
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Matches 4
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kba. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans are properly as the detection of diagnosis of N. meningitidis infection in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
            AAY57044;
                              AAY57044 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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487; Conservative
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                                                                                               ASASVGYQW 541
                                                                                                                         QAIATAGLVQAYLPGKSMMAIGGGTYLGEAGYAIGYSSISAGGNWIIKGTASGNSRGHFG
                                                                                                                                                    KDGKLYTGKGKGENGSSTDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETYT
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                                                                                                                                                                                                                                                                                                                                                                                                                          SGTKYTFASGNGTTATYSKDDQGNITYKYDVNYGDALNVNQLQNSGWNLDSKAVAGSSGK
                                                                                                                                                                                                                                                                                                                                               TDEDEEEELESVQR-SVVGSIQASMEGSVELETISLSMTNDS------KEFVDPYIVVT
                                                                                                                  QAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFG
                                                                                                                                                                                                                                                                                                                     NIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKE
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                                                                             59
                             Protein;
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88.78;
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Pred. No. 1.7e-131;
.5; Mismatches 34;
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Best Local S
Matches 487
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                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
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                                                                                                                                   487;
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 173
                   166
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                                                                                                                                             Similarity
                                                      LKAGDNLKIKQNTNENTNASSFTYSLKKDLTGLINVETEKLSFGANGKKVNIISDTKGLN 112
 NIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKE
                 TDEDEEEELESVQR-SVVGSIQASMEGSVELETISLSMTNDS-----KEFVDPYIVVT
                                                                                              TTDDDDLYLEPVQRTAVVLSFRSDKEGTGEKE-----VTEDSNWGVYFDKKGVLTAGTIT
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English.

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13-MAY-1998;
                                                            07-MAY-1999;
                                                                                            18-NOV-1999
                                                                                                                           WO9958683-A2
                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                       Neisseria
                                                                                                                                                                                                                                                                   BASB029; Nisseria meningitidis; surface fibril protein;
                                                                                                                                                                                                                                                                                                                                   21-FEB-2000
SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                    amino
                                                                                                                                                                                                                     meningitidis
                                                                                                                                                                                                                                                   treatment; prevent; antibacterial drug
                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                 acid sequence
                               98GB-0010276
                                                            99WO-EP03255
                                                                                                                                                                       Location/Qualifiers 104
                                                                                                                                                        /note=
                                                                                                                                                        "Encoded
                                                                                                                                                                                                                                                                                                  from N. meningitidis strain
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                                                                                                                                                        AATC"
                                                                                                                                                                                                                                                                     HSF; diagnosis;
                                                                                                                                                                                                                                                                                                    ATCC13090
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CC This is the Nisseria meningitidis BASB029 amino acid sequence from CC serogroup B strain ATCC13090. The BASB029 protein is homologous to the CC Haemophilus influenzae surface fibril (HSF) protein. The invention CC relates to BASB029 polynucleotide sequences (AAZ39864-Z39865) and CC polypeptide sequences (AAY57044-Y57045) and their immunogenic fragments. CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria CC meningitidis infection in a mammal. Compositions containing BASB029 CC polynucleotides and polypeptides are useful for generating an immune Cr response in an animal. A therapeutic composition comprising an antibody CC directed against BASB029 is useful in treating humans with Neisseria CC meningitidis disease. The polynucleotide is useful in the diagnosis of CC the stage of infection, type of infection, susceptibility to an CC infection which results from increased or decreased expression of the CC polynucleotide, and for therapeutic or prophylactic purposes, CC particularly genetic immunisation. Antibodies against BASB029 CC particularly bacterial infections. The protein is useful in the CC particularly bacterial infections. The protein is useful in the CC particularly bacterial infections. The protein is useful in the CC protein is useful for the stimulation of the immune system of an organism or protein. receiving the 594 AA; protein. system of an organism

Conservative

15;

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Score 2404.5; DB 2 Pred. No. 1.7e-131; 5; Mismatches 34;

21;

Length

594; 13;

Indels

Gaps

105

232

87.9%; 88.7%;

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RESULT 15
AAU06174
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213..231
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Matches 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New NhhA surface antigen polypeptides and polynucleotides
Neisseria meningitidis, useful in producing vaccines for preventing broad spectrum of Neisseria meningitidis -
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## ALIGNMENTS

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SEQ ID NO 17
LENGTH: 592
TYPE: PRT
ORGANISM: Neisseria meningitidis
US-09-377-155-17
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APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SUFFACE ANTIGEN
FILE REFERENCE: 065964/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT EILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILLING DATE: 1998-12-14
PRIOR FILLING DATE: 1997-12-12
PRIOR FILLING DATE: 1997-12-12
PRIOR FILLING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
COCTUMENT: DEPT 33
COCTUMENT: DEPT 33
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PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
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Best Local S
Matches 541
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LENGTH: 592
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Patent No. 6333173
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APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
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SGNGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSP
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Pred. No. 5.9e-208;
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CURRENT FILING DATE: 1990-08-19
PRIOR APPLICATION NUMBER: POT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 599
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US-09-377-155-15
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Best Local Sim
Matches 496;
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE AN
FILE REFERENCE: 065064/0128
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Patent No.
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                                           KDGKLYTGKGKGENGSSTDEGEGLYTAKEYIDAYNKAGWRMKTTTANGQTGQADKFETYT
                                                                                                                                        NIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKE
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VISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSV
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90.3%; Pred. No. 3.16
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CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
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TYPE: PRT
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                                                           VISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSV 412
                                                                                                                                                     KDGKLVTGKGKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVT
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                                                                                                                                                                       KDGKLYTGKGKGENGSSTDEGEGLYTAKEYIDAVNKAGWRMKTTTANGQTGQADKFETYT
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                                                                                                 SGTNVTFASGKGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGK
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Pred. No. 3.1e-185;
Pred. No. 3.3:
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; LENGTH: 598
; TYPE: PRT
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CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
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AGIAQAIATAGLVQAYLPGKSMMAIGGGTYLGEAGYAIGYSSISAGGNWIIKGTASGNSR
                                                           TLSVDDEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVNGNAR 468
                                                                                                SSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAP 408
                                                                                                                                                     NAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTS
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                                          TLSVDDEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNAR
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Pred. No. 1.4e-183;
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CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 13
LENGTH: 598

/ ORGANISM: Neisseria meningitidis
US-09-377-155-13
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US-09-377-155-13
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PRIOR FILING DATE: 1999-08-19
PRIOR PPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIA VET. 2.0
SEQ ID NO 5
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TYPE: PRT
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CURRENT FILING DATE: 2000-09-26
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US-09-669-974-13
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CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR PILING DATE: 1997-12-12
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APPLICANT: PEAK, Ia
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Similarity 89.2%; Pred. No. 1.4e-183;
93; Conservative 11; Mismatches 28;
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              RESULT 10
US-09-669-974-7
; Sequence 7, Application
; Patent No. 6333173
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CURRENT APPLICATION UNMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
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; ORGANISM: Neisseria meningitidis
US-09-377-155-7
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GENERAL INFORMATION:
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                                                                                                             ASASVGYQW
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Pred. No. 2.4e-183;
0; Mismatches 31;
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Indels Length

17;

Gaps

172 165

225

232

412

405

352 345 292 285

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525

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Indels Length

13;

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RESULT 11
US-09-377-155-9
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APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: DCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
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Best Local S
Matches 491
              Sequence 9, Application US/09377155
Patent No. 6137312
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Ansel
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PRIOR ETLING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
   APPLICANT:
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ASASVGYQW
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JENNINGS,
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 Richard Anselm
Michael Paul
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89.4%; Pred. No. 2.46
tive 10; Mismatches
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; TYPE: PRT
; ORGANISM: Neisseria
US-09-377-155-9
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Best Local S
Matches 487
                                                                                     Sequence 9, Application US/09669974 Patent No. 6333173 GENERAL INFORMATION:
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PRIOR ETILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 594
                          APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 0650 CURRENT APPLICATION
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CURRENT FILING DATE: 1999-08-19
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TITLE OF INVENTION:
FILE REFERENCE: 065
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               065064/0128
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065064/0128
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88.7%; Pred. No. 7.7e-182;
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 US/09/669,974
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US-09-377-155-21
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PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION TOMBER: GB 9726398.2
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-13-12
PRIOR FILING DATE: 1997-13-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 9
LENGTH: 59
                                                                                          Sequence 21, Application US/09377155 Patent No. 6197312 GENERAL INFORMATION:
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Matches
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APPLICANT: PEAK, Ian Richard Anselm APPLICANT: JENNINGS, Michael Paul APPLICANT: MOXON, E. Richard TITLE OF INVENTION: NOVEL SURFACE ANTIGEN CURRENT EPILCATION NUMBER: US/09/377,155 CURRENT FILLING DATE: 1999-08-19 PRIOR APPLICATION NUMBER: PCT/AU98/01031
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487; Conserv
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88.7%; Pred. No. 7.7e-182;
Live 15; Mismatches 34;
                                              SURFACE ANTIGEN
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         Sequence 21, Application US/09669974
Patent NO. 6333173
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: MOXON, E. Richard
APPLICANT: MOXON, E. RICHARD
TITLE OF INVENTION: NOVEL SUFFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT APPLICATION NUMBER: US/09/377,155
PRIOR APPLICATION NUMBER: US/09/377,155
PRIOR APPLICATION NUMBER: US/09/377,155
PRIOR APPLICATION NUMBER: US/09/377,155
PRIOR FILING DATE: 1998-08-19
PRIOR FILING DATE: 1998-12-14
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US-09-377-155-21
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US-09-669-974-21
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LENGTH: 591
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PRIOR APPLICATION NUMBER: GB 'S
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
CORTANDE BATCHIO VOE
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
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; ORGANISM: Neisseria
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NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 591
SOFTWARE:
SEQ ID NO 1
                                                                                                                                                                                     Sequence 11, Application Patent No. 6197312 GENERAL INFORMATION:
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Best Local Similarity 86.8%;
Matches 475; Conservative 2:
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                                                 ASVGYQW 541
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Pred. No. 1.9e
22; Mismatches
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Result
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4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*

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23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*

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Copyright (c) 1993 - 2003 Compugen Ltd.
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   AAU06183
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## ALIGNMENTS

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Surface antigen NhhA; meningococcal disease; meningitis vaccine; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New NhhA surface antigen polypeptides and polynucleotides Neisseria meningitidis, useful in producing vaccines for topreventing broad spectrum of Neisseria meningitidis -
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513; Conser
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                                                                                            SSISAGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                             LKGVAQNLNURIDNVNGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYLGEAGYAIGY
                                                                                                                                                                ATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQ
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AAY23744

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immunoreactive p
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  SKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
                                                             TDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTFASGNGTTATV
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Pred. No. 6.46
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237..592
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/note= "Variable region
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Best Local S
Matches 513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                  VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGKGENGSS
                                                                                                                                                                                                                                                                                                                              GIGSTLTDMLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fig 1; 91pp; English.
                                                                                                                                                                                                                      TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTFASGNGTTATV
                                                                                                                                                                                                                                                                                                                  GIGSTLTDMLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
            MMAIGGGTYLGEAGYAIGYSSISAGGNWIIKGTASGNSRGHFGASASVGYQW 513
                                                                                                                                                       SKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
                                                                                                                                                                                                                                                            VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGKGENGSS
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 MMAIGGGTYLGEAGYAIGYSSISAGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                                                                                                          TDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTFASGNGTTATV
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86.7%;
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Matches 498
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(UYQU)
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ASDNVDFVHTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKG
                 ASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKG
                                                                                                                    DTTVHLNGIGSTLTDMLLNTGATTNVTINDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTT
                                                                                                                                                                                        KNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNG
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                                                                                         DTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDKKKRAASVKDVLNAGWNIKGVKPGTT
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Pred. No. 6.2e-145;
5; Mismatches 10;
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237..243
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                 AYLPGKSMMAIGGGTYLGEAGYAIGYSSISAGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                     KDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVNGNARAGIAQAIATAGLVQ
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5.2e-145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 Kba. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in human.
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N-PSDB; AAX85794.
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                 SDNVDFVRTYDTVEELSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGK
                                                                 PTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA
                                                                                                                                     NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGD
 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGK
                                                                                 TTVHLNGIGSTLTDMLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU06177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU06177 standard; Protein;
                                                                                                                                                                                                                                                                                         Regior
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                                                                                                                                                                                                                                                                                                                                                                                                                                              antigen NhhA; meningococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLAQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DANKPYRITNVAPGVKEGDYTNVAQLKGVAQNLNNRIDNVNGNARAGIAQAIATAGLVQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTFASGN
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                                                                                                                                                                                                                                                                                                                                                                                                                         meningitidis strain H15.
            2000US-0177917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                       /label= C2
/note= "Conserved 1
117..130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H15
                                                                                                                                                                                         /note- "Variable 217..235
                                                                                                                                                                                                                                                                                                                                                        /note= "Conserved region 51..104
                                                                                                                       /label= V4
/note= "Variable region
243..598
                                                                                                                                                       /label= C4
/note= "Conserved
236..242
                                                                                                                                                                                                                                                         /note= "Variable region 131..194
                                                                                                                                                                                                                                                                                                                                  /label= V1
/note= "Variable region
                                                                                                                                                                                                                         /note= "Conserved
195..216
                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                             /label=
                                                                                                                                                                                                             /label=
                                                                                                                                                                                                                                               /label=
                                                                                                                                                                                                                                                                             /label= v2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     surface
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                                                                                                  "Conserved
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                                                                                                                                                                                                                                                                                                                                                                                                                                               disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NhhA polypeptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                              meningitis vaccine
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481 396 В Qy В

421 336

KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSK

KMDETYNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSK

DANKPYRITNYAPGYKEGDYTNYAQLKGYAQNLNNRIDNYNGNARAGIAQAIATAGLYQA

455 480 395

DANKPYRITNVAPGYKEGDYTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLAQA

GTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKG

GTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKG

420 335 360 275 300 215

GENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTFASGN

SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGK SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGK

DENGSSTDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTFASGN

Qγ

456

YLPGKSMMAIGGGTYLGEAGYAIGYSSISAGGNWIIKGTASGNSRGHFGASASVGYQW

598 513

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Qy

361 276 DЬ Qy DЬ Qy

301

216 241 156 181 Qy

96

TTVHLNGIGSTLTDMLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA 155

180 95 PVQRTAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE

54 60 54

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121

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В Qy

Query Match Best Local : Matches

Local Similarity

94.6%;

Score 2460.5; DB 2 Pred. No. 3.2e-144; 4; Mismatches 13;

DB 22;

Indels Length

85; 598;

Gaps

496;

Conservative

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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhhA (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen NhhA from N. meningitidis strain H15 is 1 of 10 NhhA polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-488774/53.
N-PSDB; AAS09167.
Sequence
                                                                                                                                                                                                                                                                                                                                                                  Claim 9; Fig 1; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                        New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYQU ) UNIV QUEENSLAND
                                        present invention.
  598 AA;
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RESULT 8
AAU06182
AAU06182
AAU06182
AAU06182
AC AAU0
AC AAU0
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FH Key
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Best Local
                                                                                                                                                                                                                                                                                                                                       The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhhA (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence represents N. meningitidis strain pMC21 surface antigen NhhA deletion mutant #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New NhhA surface antigen polypeptides and polynucleotides
Neisseria meningitidis, useful in producing vaccines for
preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peak
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                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-488774/53.
                                                                                                                                                                                                   489;
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                                                                                                                                                                                                                           Similarity
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                                                                                                                           MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLEATVQANATDETGLINV
GTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTNV
                         ETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDMLLNTGATTNV
                                                                                                 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANNETDLTSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fig 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PMC21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Signal_peptide 52..512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Mature_NhhA_deletion_mutant_#1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1..51
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                                                                                                                                                                                                                        94.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Predicted mature protein, claimed in claim 12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             strain
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                                                                                                                                                                                              Score 2456.5; DB 2
Pred. No. 4.6e-144;
5; Mismatches 18;
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                                                                                                                                                                                  Claim
                                                                                                                                                                                                                             Neisseria meningitidis surface proteins useful for treating meningitidis infections
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The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 KDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans the detection or diagnosis of N. meningitidis infection in humans the detection or diagnosis of N. meningitidis surface glycoproteins can also be used to

also be humans,

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RESULT 10
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be
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                                                                                                                                        antigen NhhA; meningococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                              KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSK 395
                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKG
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                                                                                                                                                                                                                                                                                                                                                                                  KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSK
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                                                                                                                  meningitidis strain BZ10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of vaccines. The proteins and antibodies identify immunoreactive peptides.
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                                                                                                                                                                BZ10
                                               /note= "Conserved 51..104
             /label= V1
/note= "Variable region
105..116
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                                                                                          Location/Qualifiers
                                                                      /label=
                                                                                                                                                              surface antigen NhhA polypeptide sequence
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PVQRTAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE

120

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180 95

55 61 55 Local Similarity

94.2%; 82.6%;

Score 2451.5; Pred. No. 1.1e 5; Mismatches

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Query Match
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                                                                   The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhhA (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strains given in (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                   Sequence
                                                                                                                                                                                                                                              Claim 9;
                                                                                                                                                                                                                                                                                                                     WPI; 2001-488774/53.
N-PSDB; AAS09168.
                                                                                                                                                                                                                                                                   New NhhA surface antigen polypeptides and polynucleotides Neisseria meningitidis, useful in producing vaccines for the preventing broad spectrum of Neisseria meningitidis.
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/note= "Variable
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        meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans The N. meningitidis surface glycoproteins can alone the contract of the co
                                                                                                                              Claim 1;
                                                                                                                                                            Neisseria meningitidis surface proteins useful meningitidis infections
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                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New NhhA surface antigen polypeptides and polynucleotides Neisseria meningitidis, useful in producing vaccines for preventing broad spectrum of Neisseria meningitidis -
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Pred. No. 1.7e-143;
                                                                                                                                                                                                                         Mismatches
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surface glycoproteins, nucleic acids, the primers and optic a thermostable polymerase, or antibodies are useful in a k: the detection or diagnosis of N. meningitidis infection in
                                                                The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis
                                                                                                                  Claim 1;
                                                                                                                                                  Neisseria meningitidis surface meningitidis infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Surface protein;
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                                                WO9958683-A2
                                                                                           Misc-difference
                                                                                                                                      Neisseria
                                                                                                                                                                             BASB029; Nisseria meningitidis; surface fibril protein;
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Pred. No. 4.5e-141;
7; Mismatches 19;
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                                            TVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE
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                                                         TVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE
                                                                                                    SSTDKGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETYTSGTNYTFASGKGTTA
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     New NhhA surface antigen polypeptides and polynucleotides
Neisseria meningitidis, useful in producing vaccines for 1
preventing broad spectrum of Neisseria meningitidis -
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KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                       PVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVNGNARAGIAQAIATAGLVQAYLPG
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(without alignments)
1582.188 Million cell updates
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SEQ ID NO 17
LENGTH: 592
TYPE: PRT
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Best Local Similarity
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NUMBER OF SEQ ID NOS:
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21.6	25.7	26.3	29.2	29.2	33.9	33.9	33.9	33.9	33.9	36.1	36.1	36.1	36.1	36.2	37.0	37.0	37.0
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Sequence :	Sequence :	Sequence :	Sequence 2	Sequence :	Sequence '	Sequence '	Sequence (	Sequence (	Sequence (	Sequence '	Sequence	Sequence '	Sequence 3	Sequence :	Sequence !	Sequence :	Sequence :
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App	App	App	App	App	Appl	Appl:	Appl	Appl	Appl	App	App	Appl	App	App	App1:	Appl	Appl

## ALIGNMENTS

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; ORGANISM: Neisseria meningitidis US-09-377-155-17
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CURRENT APPLICATION NUMBER: US/09/377,155

CURRENT FILING DATE: 1999-08-19
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PRIOR FILING DATE: 1997-12-12
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PRIOR FILING DATE: 1998-12-14
222 TDEGEGLUTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTFASGNGTTATV
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                                                           VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGKGENGSS
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CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1999-12-12
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
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US-09-669-974-17
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SEQ ID NO 17
LENGTH: 592
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                                                                      VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGKGENGSS
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  TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTFASGNGTTATV
                                                        VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGKGENGSS
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Pred. No. 8.8e-196;
0; Mismatches 0;
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US-09-377-155-15
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SOFTWARE: PatentIn Ver.
SEQ ID NO 15
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Best Local
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CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 199-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
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TYPE: PRT
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                                                        KGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASG
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; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria m
US-09-669-974-15
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APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: DCT/AU98/01031
PRIOR APPLICATION NUMBER: CB 9726398.2
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: CB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
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                                                        NGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSK 334
                                                                                                              KGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTFASG
                                                                                                                                                       ASDNVDFVHTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKG
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               GKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGS
                                           KGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSK
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Pred. No. 2.4e-189;
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US-09-377-155-13
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Matches 496;
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SEQ ID NO 13
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APPLICANT:
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APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SUI
FILE REFERENCE: 065064/0128
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CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
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DANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVNGNARAGIAQAIATAGLVQA
                                                        KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSK
                                                                                                              GTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKG
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Pred. No. 2e-188;
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US-09-669-974-13
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CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
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             DANKPYRITNVAPGYKEGDVTNVAQLKGVAQNLNNRIDNVNGNARAGIAQAIATAGLVQA
                                                                       KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSK
                                                                                                                 GTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKG
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DANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLAQA
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Pred. No. 2e-188;
4; Mismatches 13
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Matches 494
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APPLICANT: PERK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
APPLICANT: MOXON, E. RICHARD
TITLE OF INVENTION: NOVEL SURFACE A
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LENGTH: 598
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CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
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SOFTWARE: PatentIn Ve
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                                                                       DANKPYRITNYAPGYKEGDYTNYAQLKGVAQNLNNRIDNYNGNARAGIAQAIATAGLYQA 455
                                                                                                              KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSK 395
                                                                                                                                                                      SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGK 215
                                                                                                                                                                                                                                                                                                                                                                 TTVHLNGIGSTLTDMLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA 155
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YLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGTSASVGYQW
                                                         DANKPYRITNVAPGYKEGDYTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLAQA
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Pred. No. 1e-187;
5; Mismatches 14;
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US-09-669-974-5
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Best Local
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CURRENT APPLICATION NUMBER: US/09/669,974

CURRENT FILING DATE: 2000-99-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR PLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
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                                                                                                          KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSK
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              YLPGKSMMAIGGGTYLGEAGYAIGYSSISAGGNWIIKGTASGNSRGHFGASASVGYQW 513
                                                                    DANKPYRITNYAPGYKEGDYTNYAQLKGVAQNLNNRIDNYNGNARAGIAQAIATAGLVQA 455
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                                                     DANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLAQA
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Pred. No. 1e-187;
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RESULT 10
US-09-669-974-7
; Sequence 7, Application
; Patent No. 6333173
; GENERAL INFORMATION:

US/09669974

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; TYPE: PAT
; ORGANISM: Neisseria meningitidis
US-09-377-155-7
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APPLICANT: MOXON, E. RiCHARD
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
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SEQ ID NO 7
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PatentIn Ver. 2.0
                                                                                                   SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTFASGNGTTA
                                                                                                                                                                                                                                                               LNGIGSTLTDMLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV 159
             KSMMAIGGGTYLGEAGYAIGYSSISAGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                                                                                                                                                                                                                                                                      NTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGDPTVH
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KSMMAIGGDTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                 PVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPG
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Pred. No. 1.8e
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RESULT 11
US-09-377-155-9
US-09-377-155-9; Sequence 9, Application U; Patent No. 6197312; GENERAL INFORMATION: APPLICANT: PEAK, Ian R1; APPLICANT: JENNINGS, M1;
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CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
VUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 7
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TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
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ORGANISM: Neisseria
09-669-974-7
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JENNINGS, Michael Paul
MOXON, E. Richard
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83.2%;
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Pred. No. 1.8e
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RESULT 12 US-09-669-974-9

Sequence 9, Application US/09669974
Patent NO. 6333173
GEMERRAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128

NUMBER: US/09/669,974

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US-09-377-155-9
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SOFTWARE: PatentIn Vei
SEQ ID NO 9
LENGTH: 594
TYPE: PRT
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COURRENT APPLICATION NUMBER: US/09
COURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AL
PRIOR ETLING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 97
PRIOR FILING DATE: 1997-12-12
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Best Local :
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                                                    PVRITNVAPGYKEGDYTNVAQLKGYAQNLNNRIDNVNGNARAGIAQAIATAGLVQAYLPG
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                                            PVRITNVAPGVKEGDVTNVAQLKGVAQNLNNHIDNVDGNARAGIAQAIATAGLVQAYLPG
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Pred. No. 2.3e-184;
7; Mismatches 19;
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; TYPE: PRT ; ORGANISM: Neisseria meningitidis US-09-669-974-9
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; Sequence 21, Application
; Patent No. 6197312
; GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
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                                 APPLICANT: PEAK, Ian Richard Anselm APPLICANT: JENNINGS, Michael Paul APPLICANT: MOXON, E. Richard TITLE OF INVENTION: NOVEL SURFACE ALFILE REFERENCE: 065064/0128
             CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
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                                               SURFACE ANTIGEN
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Pred. No. 2.3e-184;
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                                                                             ; Sequence 21, Application US/09669974
patent No. 6333173
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE AN
FILE REFERENCE: 065064/0128
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PRIOR APPLICATION NUMBER: GB 972
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 591
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US-09-377-155-21
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Matches
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR ETIING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
                                                        CURRENT APPLICATION NUMBER: US/09/669,974 CURRENT FILING DATE: 2000-09-26
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
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US-09-377-155-2
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                                                                                                                                                                               Sequence 2, Application US/09377155 Patent No. 6197312 GENERAL INFORMATION:
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Pred. No. 3.7e-184;
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; TYPE: PRT
; ORGANISM: Neisseria
US-09-377-155-2
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VNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKP
                                                                                                     VNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSKKDNKP
                                                                                                                                         STDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTAT
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5; Mismatches
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Search co completed: October ne : 15.7186 secs 6 2003, 09:35:42

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180.5	180.5	180.5	181	181.5	182	182.5	182.5	184	184.5	185	187	187	187.5	188	189.5
6.9	6.9	6.9	7.0	7.0	7.0	7.0	7.0	7.1	7.1	7.1	7.2	7.2	7.2	7.2	7.3
1270	1268	893	1366	1275	1655	1109	1004	2551	1417	4152	3013	961	365	2020	2468
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E85649	в99789	A37284	S57664	T33369	E97835	A56143	T00046	B98047	A83080	T31102	AB0480	AD0548	AB3486	C48399	A83412
hypothetical prote	hemagglutinin/hemo	surface-array prot	IgA-specific metal	hypothetical prote	hypothetical prote	surface-array prot	surface layer prot	hypothetical prote	hypothetical prote	filamentous hemagg	probable invasin Y	puative autotransp	cell surface prote	ABC-type transport	hypothetical prote

## ALIGNMENTS

adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001
C;Accession: G81133
C;Accession: G81133
R;Tettelin, H; Saunders, N.J.; Heidelberg, J; Jeffries, A.C.; Nelson, K.E.; Elsen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.
ri, H; Qin, H; Vamathevan, J; Gill, J; Scarlato, V; Masignani, V; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandl, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: G81133
A;Status: preliminary
A;Rolecule type: DNA
A;Residues: 1-591 <TETS
A;Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAF41395.1; PID:g722
A;Experimental source: serogroup B, Strain MC58 SKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTFASGNGTTATV TDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV Score 2407; DB 2; Pred. No. 2.7e-118; 5; Mismatches 18; Length Indels ; 08 Gaps 161 180 101 120 60 341 281 221 240 300 54

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probable surface fibril protein NMA1200 [imported] - Neisseri C:Species: Neisseria meningitidis C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_chan C:Accession: A81888
R:Parkhill, J:; Achtman, M.; James, K.D.; Bentley, S.D.; Chur Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K. Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Nei A:Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: A818888
A;Status: preliminary A;Mclecule type: DNA A;Residues: 1-592 cparb
A;Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PA:Experimental source: serogroup A, strain Z2491
C;Genetics: NMA1200
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                                      TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANK
                                                                                                       TVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE
                                                                                                                                                            SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTFASGNGTTA
                                                                                                                                                                                                    GIGSTLIDMLLNTGATINVINDNVIDDEKKRAASVKDVLNAGWNIKGVKPGTTA--SDNV
                                                                                           TVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE
                                                                                                                                               {\tt SSTDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA}
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            PVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVNGNARAGIAQAIATAGLVQAYLPG
                                                                                                                                                                                                                                                         GIGSTLTDTLAGSSASHVDAGNQST--HYTRAASIKDVLNAGWNIKGVKTGSTTGQSENV
                                                                                                                                                                                                                                                                                                             NASSFTYSLKKDLTGLINVETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN
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Pred. No. 2.1e
9; Mismatches
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2.1e-115;
les 22;
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Mungall, K.; Quail,
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M.A.;
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A; Residues: 1-298 <TIGR>
A; Cross-references: GB:U
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  14
23
  .5%;
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adhesin homolog HII732 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Oct-1997
C;Accession: I64138
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerl; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; We, D.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae R. A;Title: Whole-genome random sequencing and assembly of A;Accession: I64138
A;Ratession: I64138
A;Status: nucleic_acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQA---
TGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSA 173
                                                                                                                                                                                                                   VSDTLTIGGNTPAAGGATPKVSITSTADGLKLAK - - - GTNGDTAVHLNGLASTLPDVTTN
                                                                                                                                                                                                                                                                                                                            STEDDIEDSAATKDDNKNQALKAGDTLTLKAGKNLKAKLDQGGKSVTFALAKDLDVKTAK
                                                                                                                                                                                                                                                                                                                                                                                                                                  MNKIFKVIWNVVTQTWVVVSELTRAHTKRTSATVATAVLATVLSATVQAINDAGTFVKVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KSMMAIGGGTYLGEAGYAIGYSSISAGGNWIIKGTASGNSRGHFGASASVGYQW
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                                                                                                           TGASTSVT-FSPSDIEKTRAATIKDVLNAGWNIKGAKVAGGNTENVDLVAGYDNVEFITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB:U32846; GB:L42023; NID:g1574588; PID:g1574589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.2%;
43.1%;
                                                                                                                                                                                                                                                                                                                                                                                  -----NATDETGL----
                                                                                                                                                                                                                                                                 FGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDMLLN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28;
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Pred.
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No. 1.1
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1.; Weidman
Jen, N.S.M.
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A; McCessaco... A; Status: preliminary A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-1588 <5TO> A; Cross-references: GB: AE005174; NID: g12518349; PIDN: AAG58749.1; GSPDB: GN00145; A; Cross-references: GB: AE005174; NID: g12518349; PIDN: AAG58749.1; GSPDB: GN00145; NID: Cross-references: GB: AE005174; NID: g12518349; PIDN: AAG58749.1; GSPDB: GN00145; NID: Cross-references: GB: AE005174; NID: g12518349; PIDN: AAG58749.1; GSPDB: GN00145; NID: Cross-references: GB: AE005174; NID: g12518349; PIDN: AAG58749.1; GSPDB: GN00145; NID: Cross-references: GB: AE005174; NID: g12518349; PIDN: AAG58749.1; GSPDB: GN00145; NID: Cross-references: GB: AE005174; NID: g12518349; PIDN: AAG58749.1; GSPDB: GN00145; NID: Cross-references: GB: AE005174; NID: g12518349; PIDN: AAG58749.1; GSPDB: GN00145; NID: Cross-references: GB: AE005174; NID: g12518349; PIDN: AAG58749.1; GSPDB: GN00145; NID: Cross-references: GB: AE005174; NID: g12518349; PIDN: AAG58749.1; GSPDB: GN00145; NID: Cross-references: GB: AE005174; NID: g12518349; PIDN: AAG58749.1; GSPDB: GN00145; NID: Cross-references: GB: AE005174; NID: g12518349; PIDN: AAG58749.1; GSPDB: GN00145; NID: GN00145; N probable adhesin Z5029 [imported] - Escherichia coli (strain 0157:H7, subst C; Species: Escherichia coli C; Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001 C; Accession: A86036 R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001 A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7. A; Reference number: A85480; MUID:21074935; PMID:11206551 A; Accession: A86036 М., .; мау Apoda OWGP

substrain

EDL93

Score Pred.

371; No. 1

DB 2; .2e-11;

Length

Qy	Query Ma Best Loc Matches	A; Molecule A; Molecule A; Residues: A; Cross-ref A; Experimen C; Genetics: A; Gene: ECs	A; Title: A; Refere A; Access	R;Hayashi, gasawara, DNA Res. 8	RESULT 5 H91188 probable C; Species C; Date: 1 C: Access	Qy Db	Qy	Qy Db	Qy Db	ОУ Db	Qу	Qy Db	Qy Db	Qy Db	Qу Db	Qy Db	Matches
7 IIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATD 53	/ Match . 14.3%; Score 371; DB 2; Length 1588; Local Similarity 23.5%; Pred. No. 1.2e-11; res 148; Conservative 84; Mismatches 258; Indels 140; Gaps 20;	Molecule type: DNA Molecule type: DNA Residues: 1-1588 <hay> Cross references: GB:BA000007; PIDN:BAB37903.1; PID:913363955; GSPDB:GN00154 Experimental source: strain 0157:H7, substrain RIMD 0509952 Genetics: Gene: ECs4480</hay>	complete on the number on: H9118	10. 171100 11. T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. , N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. 8, 11-22. 2001	ESUTY 5 191188 191188 192188 193188 1	484 SAGGNWIKGTASGNSRGHFGASASVGYQW 513        :         :   :         1559 SANGRWYKLOGSTNSQGEYSAALGAGIQW 1588	427NINNRIDNVNGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYLGEAGYAIGYSSI 483 	375 AGADAPILSVDDEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQ 426	321 SSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLG 374	276 GTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAG 320	223 DEGEGLVTAKEVIDAVNKAGWRMKTTJANGQTGQADKFETVTSGTKVTFASGN 275	190KTEVKIGAKTSVIKEKDGKLVTGKGKGENGSST 222 :	136 VKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGK 189 :	104TDDEKKRAAS 135	54ETGLINYETEKLSFGANGKKVNII-SDTKGLNFAKETAGTNGDTTVHLNGI 103	7 IIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATD 53 :: :	s 148; Conservative 84; Mismatches 258; Indels 140; Gaps 20;
A;Authors M.; Tsuha A;Referen	A; Authors: , F.G.; Nu Rodrigues,	40.40884	A; Molecule A; Residues A; Cross-re	A; Reference A; Note: fo A; Accession A: Status:	Spec. Date Acces Acces anony ture ture	RESULT   A82615	Qу	Qy	Qу	Qy	Qу	Qy	Qy	Qy	Qy .	Оy	Db
Authors: da Silva, A.C.K.; da Silva, F.K.; da Silva, A.M.; Silva Jr., W.A.; da Silv ; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L. Reference number: A59328	M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins prs: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Nes, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa	្រុក ខ្លួក ក្រុក ខ្លួក ក្រុក	. FIGURE DAA ule type: DAA ues: 1-1190 <sim> -references: GB:AE004017; GB:AE003849; NID:g9107083; PIDN:AAF84783.1; GSPDB:GN</sim>	ence number: A82515; MULD:2036717; PMLD:10347 for a complete list of authors see reference number A59328 below sion: A82615 s. preliminary	ies: Xylella fastidiosa :18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 ssion: A82615 gmous, The xylella fastidiosa Consortium of the Organization for Nucleotide Seq 406, 151-157, 2000 2015 The genome sequence of the plant pathogen xylella fastidiosa.		484 SAGGNWIIKGTASGNSRGHFGASASVGYQW 513 	427NLNNRIDNVNGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYLGEAGYAIGYSSI 483 	375 AGADAPTLSVDDEGALNVGSKDANKÞVRITNVAÞGVKEGDVTNVAÐLKGVAÐ 426	321 SSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPOFSSVSLG 374 	276 GTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAG 320   :::	223 DEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTFASGN 275 	190KTEVKIGAKTSVIKEKDGKLVTGKGKGENGSST 222 : :     :	136 VKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGK 189 	104GSTLTDMLLNTGA-TTNVTNDNVTDDEKKRAAS 135	54ETGLINVETEKLSFGANGKKVNII-SDTKGLNFAKETAGTNGDTTVHLNGI 103   :	976 LLWDETANGGAGAYNASHDGKASIITNVANGSISEDSTDAVNGSQLNATNMM 1027

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th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dow
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Status: preliminary
                                                                                                                                                                                                                                                 probable autotransporter sapB [imported] - Salmonella enterica subsp. C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov C;Accession: AC0976
R;Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; W R;Parkhill, J.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.;
                                                                                                  A; Molecule type: Di
A; Residues: 1-1107
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AC0976
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                                                                   A;Cross-references: GB:AL513382; C;Genetics:
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 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLSVDDEGAL------NVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VAVSELTRNHTKRASATVKTAVLATLLFATVQANATDETGLINVETEKLSFGAN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SASADNAVAIGNHSVADRANTVSVGSAGSER--QVTNVAAGTADTDAVNVSQLNQGLITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVTLGSMGLVITDGPSVTSSGI----NAGSQKITNVAAGTADTDAVNLSQLNTAMAGSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATTNVTNDNVTDDEKKRAASVKDVLNAG-WNIKGVKPGTTASD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GESVDLKNTDGNIVISKESGSNDVLFNLSSSLKLDKLTVGDTVMTTNGV-----TVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKKVNIISDTKGLNFAKETAG------TNGDTTVHLNGIGSTLTDMLLNT
                                                                                                                                                                                                                                                                                                                                                                                                                                            ESGRWVFKFSGSANTRSQVGIGAGVGYQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KQYTDGVVGSLRRDTDGGVAAAIATANLPQAYIPGRGMTSVGVSSYRGQSAIAVGVSSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNRIDNVNGNAR----AGIAQAIATAGLVQAYLPGKSMMAIGGGTYLGEAGYAIGYSSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----VKVNSLNN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADA------P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTATYSKDDQGNITYKYDVNVGDALNVNQL----QNSGWNLDSKAVAGSSGKVISGNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASGKGSTAIGRNAVASADGSVALGD-GAKDGARGAESYTGKYSGLQNNTVGTVSVGDASK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENG-SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTFASGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KSVHYYSTYD-----GGTQGGNYNGDGATGTRSIAVGVGTLASA----EGATAVGSGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -NVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGKG
                                                                                                                        DNA
                                                                                                    <PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - NVADAKEAT - - DAVNLRQLDRVAQDANRYVDNKIESLSEGQTF - - - -
 13
21
 .9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83;
                                                                                  PIDN:CAD03303.1;
 Score
Pred.
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Pred. No. 1.7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----SATPIAAGVDATAIGVGATASGADSIAMGNKA 1043
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361;
No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            1190
 DB 2;
.5e-11;
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                                                                                  PID:g16504923; GSPDB:GN00176
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                                                                                                                                                                                     Skelton, J. Salmonella
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                                                                                                                                                                                                                                                        Wain, J.; White,
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                                              SAMAMAGLPQAYAPGANMTSIAGGTFNGESAVAIGVSMVSESGGWVYKLQGTSNSQGDYS
                                                                     QAIATAGLVQAYLPGKSMMAIGGGTYLGEAGYAIGYSSISAGGNWIIKGTASGNSRGHFG
                                                                                              GSGGTTRIGNVSAAVNDTDAVNYAQLKRSVEEANTYTDQKMGEMNSKIKGIENKMSGGIA
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AAIGAGFQW
                       ASASVGYQW
                                                                                                                                              TVSVGSSTQQR--RITNVAAGVNNTDAVNVAQLKASEAGSVRYETNADGSVNYSVLNLGD
                                                                                                                                                                       ALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLK-----
                                                                                                                                                                                               IENGIGDIVTTGSTKYFKTNTDGADANAQGADSVAIGSGSIAAAENSVALGTNSVADEAN
                                                                                                                                                                                                                        -----DIATSMTPQF---
                                                                                                                                                                                                                                               FSVGSEDGQRQITNVAAGSADTDAVNVGQLKVTDAQVSRNTQSITNLNTQVSNLDTRVTN
                                                                                                                                                                                                                                                                       -SKGKMD---ETVNINAGN----
                                                                                                                                                                                                                                                                                               GIGLNTLYMADAINGIAIGSNARANHANSIAMGNGSQTTRGAQTDYTAYNMDTPQNSVGE
                                                                                                                                                                                                                                                                                                                                                QDAVTVRQLQNAIGAVTTTPTKYYHANSTEEDSLAVGTDSLAMGAK-----TIVNADAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                TENGTGVKYIRTNDNGLEGQDAYATGNGATAVGYDAVASGAGCLALGQNSSSSIEGSIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FSASHGTSGTNKITNVAAGEIASDSTDAINGSQLYETNMLISQYNESISQLAGDTSETYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASVKDVLNAGWNIKGVKPGTTASDNVDFV---RTYDT-----VEFLSADTKTTTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -VESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKG---KGENGSSTDEG----
                       513
                                                                                                                       ----GVAQ-------NLNNRIDNVNGNARAGIA
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                                                                                                                                                                                                                                                                                                                                                                     -ADKFETVTSGTKVTFASGNGTTATVSKDDQGNITVKYDVNV
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RESULT 8

D85671

Surface protein XF1529 [imported] - Xylella fastidiosa (strain 9a5c)

C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: D82671

R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucl
Nature 406, 151-157, 2000
A;Fitle: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID: 20365717; PMID: 10910347
A;Rote: for a complete list of authors see reference number A59328 below
A;Accession: D82671
A;Status: preliminary
A;Molecule type: DNA
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Nucleotide

Seq

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A;Residues: 1-2059 <SIM>
A;Cross-references: GB:AE003982; GB:AE003849; NID:g9106554; PIDN:AAF84338.1; GSPDB:GN001
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Abriones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, Has-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohn J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigu Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.H.F.; Marino, C.L.; Marques, M.Y.; Martins, E.A., Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menok, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.R. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Authors: da Silva, A.C.; de N.; Wallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A., R.G.; Santelli, R.V.; Sawasak A; Authors: da Silva, A.C.; de Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A., Reference number: A59328
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C; Species:
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Matches 151
     surface protein
s: Yersinia pesti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QAVQSVTVKATRYYSTNDGGTQGGNYDGDGATGSKAIAAGVGTQASGEGAAAVGSGAAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVIDAVNKAGWRMKTTTANGQTG------QADKFETVTSGTKVT-----FAS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VNTDGVKVG--SDVSLGAMGLFIANGPSVTASGFNAGDKVISHVAVGMADTDAVNVSQLK 1707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TDML------LNTGA--TTNVT-----NDNVTDDEKKRAASVKDVLN 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NTQLDK-----DGVKVSSNVLLDSNELVITSHSSTSSVKTLANGESVVNRTVVNGDGVNI 1532
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                                                                                                                                                     NTRSHVGVGAGVGYQW
                                                                                                                                                                                                                                                                       ---AGIAQAIATAGLVQAYLPGKSMMAIGGGTYLGEAGYAIGYSSISAGGNWIIKGTASG 497
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                                                                                                                                                                                                   NSRGHFGASASVGYQW
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     pestis
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                           (partial) YP00902 [imported] -
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                           (strain
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                           C092)
hypothetical protein b2000 - Escherichia coli (strain K-12) C; Species: Escherichia coli C; Species: Escherichia coli C; Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002 C; Accession: G64964 C; Accession: F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; F.A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                RESULT
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A; Molecule type: DNA A; Residues: 1-658 < KUR> A; Residues: 1-658 < KUR> A; Cross-references: GB: AL590842; PIDN: CAC89747.1; PID: g15978974; GSPDB: GN00175 C; Genetics: A; Gene: YP00902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change C;Accession: AHO110 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Genome sequence of Yersinia pestis, the causative A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AH0110 .
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142; Conserv
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                                           GHFGASASVGYQW
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GDFGIGVGVGYQW
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                                                                                                                                   AGIAQAIATAGLVQAYLPGKSMMAIGGGTYLGEAGYAIGYSSISAGGNWIIKGTASGNSR 500
                                                                                                                                                                                    VGSVGNER - - QITNVAPATQGTDAVNFDQLKSISNQTNAYTNQRYSELKQDLRKQNSVLS
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V.; Riley,

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Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Accession: G64964
A; Status: nucleic acid sequence•not shown; translation not show A; Molecule type: DNA
A; Residues: 1-1091 <BLAT>
A; Cross-references: GB:AE000291; GB:U00096; NID:91788298; PIDN: A; Cross-references: GB:AE000291; Substrain MG1655
C; Keywords: nucleotide binding; P-loop
F; 683-690/Region: nucleotide-binding motif A (P-loop)
A;Title: The genome sequence of the plant pathogen Xylella A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A;Accession: C82672
                                                     R;anonymous, The Xylella fastidiosa Nature 406, 151-157, 2000
                                                                               C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision
C;Accession: C82672
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                                                                                                                        outer membrane protein
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A;Status: preliminary
A;Molecule type: DNA
A;Molecu
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SVSLGFNSFVRQSGEHGVALGTDAGVSGKDSIALGY
                                                                                            SISAGGNWIIK----
                                                                                                                                                                                                                                                                           I - - - ATAGLVQAYLPGKSMMAIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGLNF-----AKETAGTNGDTTVHLNGIGSTLTDMLLNTGATTNVTN------DNVTD
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                                                                                                                                                                               IGKDSTATGASAQAVGDSSVALGTRATANAIGSSVLGVDSRARGINSTALGRQSNAIGDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -DAVNKAGWRMKTTTANGQTGQADKFETV--TSGTKVTFASGNGTTAT-VS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -LGARSRANAIGSSALGVDGHALGANSTALGGQSTAISEGGTSLG--
                                                                                       -GTASGNSRGHFGA-SASVGY
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ydek protein - Escherichia coli (Straum N-12),
N;Alternate names: protein T
C:Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: A64905; I52440; S34315
C;Accession: A64905; I52440; S34315
R;Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; |
R;Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; |
A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-1325 <BLATY
A; Cross-references: GB:AED00248; GB:U00096; NID:g1787783; PIDN:AAC74583.1; PI
A; Cross-references: GB:AED00248; GB:U00096; NID:g1787783; PIDN:AAC74583.1; PI
A; Experimental source: strain K-12, substrain MG1655
R; Cartwright, P.; Timms, M.; Lithgow, T.; Hoj, P.; Hoogenraad, N.
Biochim. Biophys. Acta 1153, 345-347, 1993
A; Title: An Escherichia coli gene showing a potential ancestral relationship
A; Reference number: 152440; MUID:94100243; PMID:8274505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Keywords: nucleous; 712-719/Region:
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A;Residues: 689-883,'K',885-1316,'S',1318-1325 <RES>
A;Cross-references: EMBL:X73295; NID:g312392; PIDN:CAA51730.1; PID:g312393
A;Note: the difference in length is due to a frameshift error at pos 653
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A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
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A;Title: The complete genome sequence of Escherichia coli A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: A64905
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                               NAGN-----NIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNV-----
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                                                                                                                                                                RMKTTTANGQTGQADKFETVTSGTKVTFASGNGTTATVSKDDQGNITVK-YD-VNVGDAL
                                                                                                                                                                                                                                VKIGAKTSVIKEKDGK-LVTGK------GKGENGSSTDEGEGLVTAKEVIDAVNKAGW
                                                                                                                                                                                                                                                                     LRLGSSTGGV--GTVNVEGEDSVLTTELFEIGSYGTGSLNIT----DKGYVTSSIVAILG
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                                                                                                                                 ---IGTLNVQ----DQDSVITVRRLYNGYFGNG---TVNISNNGLINNKEYSLVGVQDGS
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nucleotide-binding motif A
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Pred. No. 0.00019;
55; Mismatches 245
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AVAKSNSPVTFHKLTTTNLTGQGGTINMRVRLDGSNASDQLVINGGQATGKTWLAFTNVG
                               AIATAG------LVQAYLPGK-----
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-949 <HANY
A;Cross-references: GB:BA000007; PIDN:BAB34819.1; PID:g13360856; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia
A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AidA-I adhesin-like protein [imported] - Escherichia coli (strai C;Species: Escherichia coli (c;Species: Escherichia coli (c;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change C;Pate: 18-Jul-2003 #sequence_revision 18-Jul-2001 #text_change C;Accession: D90803 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
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L1-22, 2001
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                                                                                                                                                                                                                                                                                                           KAGGAAGNTTINQNGELRVHAGGEATAVTQNTGGALVT----STAATVIGTNRLGNFTV
                                                                                                                                                                                                                                                                                                                                                                                                                                        TEVKIG-AKTSVIKEKDGKLVTGKGKG---ENGSSTDEGEGLVTAKEVIDAVNKAGWRM- 245
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                                                                                                  -IADSGATVE-GTNASGKFSIDGTSGQASGLLLENGGSFTVNAGGQAGNTTVGHRGTLTL
                                                                                                                                                 EITRNGKNIDIATSMTPQFS--
                                                                                                                                                                                                    ENGKADGVVL-----ESGGRLDVLESHSAQNTLVDDGGTLAVSAGGKATSVTITSGGAL
                                                                                                                                                                                                                                                      KYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVI--SGNVSPSKGKMDETVNINAGNNI
                                                                                                                                                                                                                                                                                                                                                                                                              IILFSGLARDTLIYAGGDQSVHGRALNTTLNGGYQYVHRDGLA----LNTVINEGGWQVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGGLATGTIINTG-----AEGGPDSDN----SY-TGQKVQGTAESTTIN----KNGRQ
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                                             -GSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVNGNARAGIAQ
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                                                                                                                                                                                                                                                                                                                                   KTTTANGQT-----GQADKFETVTSGTKVTFASGNGTTATVSKDDQ-GNITV
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21.7%;
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Pred. No. 0.00034;
0; Mismatches 224;
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                                                                                                                                                 -SVSLGAGADAPTLSVDDEGALNV
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M.; Shinagawa,
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----SMMAIGGGTYLGEAGYA---IG

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A; Declar type: DNA
A; Molecule type: DNA
A; Residues: 1-1005 <STO>
A; Cross-references: GB: AE005174; NID: g12514025; PIDN: AAG55356.1;
A; Cross-references: Strain O157: H7, substrain EDL933
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C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision
C;Accession: H85611; B85663
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A;Gene: Z1211;
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A;Accession: B85663
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1005 <ST2>
A;Cross-references: GB:AE005174; NID:g12514546; PIDN:AAG55766.1; GSPDB:GN00145; UWGP:Z1/A;Experimental source: strain O157:H7, substrain EDL933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Nature 409, 529-533, 2001
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Best Local S
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     AIATAG----
|:| :
                                                          AAGGSLSGRTQLSKGASMVLNGDVVSTGDIVNAGEI-
                                                                                                                                                                                                                                    KYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVI--SGNVSPSKGKMDETVNINAGNNI
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                                                                                                                                - IADSGATVE-GTNASGKFSIDGTSGQASGLLLENGGSFTVNAGGQAGNTTVGHRGTLTL
                                                                                                                                                                    ETTRNGKNIDIATSMTPQFS-----
                                                                                                                                                                                                       ENGKADGVVL-----ESGGRLDVLESHSAQNTLVDDGGTLAVSAGGKATSVTITSGGAL
                                                                                                                                                                                                                                                                           KAGGAAGNTTINQNGELRVHAGGEATAVTQNTGGALVT----STAATVIGTNRLGNFTV
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                                                                                                                                                                                                                                                                                                                                                                                                                         SGGLATGTIINTG-----AEGGPDSDN----SY-TGQKVQGTAESTTIN----KNGRQ
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                                                                                          -GSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVNGNARAGIAQ
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21.7%;
                    -LVQAYLPGK
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Pred.
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red. No. 0.00
Mismatches
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                                                                                                                                                                    SVSLGAGADAPTLSVDDEGALNV
 -SMMAIGGGTYLGEAGYA--
                                                        ------RFDN-QTTPNAALSR
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K.; Af
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1286 <BEN>
A; Cross-references: EMBL: X65022; NID: 942254;
A; Cross-references: EMBL: X65022; NID: 942254;
R; Benz, I.; Schmidt, M.A.
R; Benz, I.; Schmidt, M.A.
A; Arnain involved in dif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Suhr, M.; Benz, I.; Schmidt, M.A.
Mol. Microbiol. 22, 31-42, 1996
A;Title: Processing of the AIDA-I precursor: removal of A;Reference number: S72657; MUID:97055419; PMID:8899706
A;Accession: S72657
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$28634
$28634
adhesin AIDA-I precursor - Escherichia coli plasmid
C;Species: Escherichia coli
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993
C;Accession: $28634; $22680; $28881; $72657
R;Benz, I.
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C;Keywords: membrane protein
F;11-49/Domain: signal sequence #status predicted <SIG>
F;50-1286/Product: adhesin AIDA-I #status predicted <M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Microbiol. 6, 1539-1546, 1992
A;Title: AIDA-I, the adhesin involved in diffuse adherence
A;Reference number: S22680; MUID:92326638; PMID:1625582
A;Accession: S22680
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A; Residues: 50-5
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A; Residues: 839-1286 <BE2>
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Best Local :
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                                                                                                             GHASNTVIFSGGNQTIFSGGITDSTNISSGGQQRVSSGGVASNTTINSSGAQNILSEEGA
                                                                                                                                                                                                         LNTGATTNVT-NDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTAS------DNV-DF
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78. 61530; 61530; (1989). (1989). (ch G.M. d obser:	8503; III, B] Glasne atricle e of H e of H mina T Takeda Takeda e Escl	P 41; d) d) equ nno (F1 (F1	Y456_CHLTR YMJB_CAEEL IGA2_HAEIN IGA2_HAEIN NH11_CHLPN YS89_CAEEL P60_LISMO APMU_PIG ICEV_PSESX ICEN_PSESX ICEN_PSESX TIEE6_STRPY HPI2_DEIRA
EMBL/GenBank/DDBJ databases.  8.  1530;  sequence of the alpha subunassociated with the outer me associated with the outer me 1989).  8646; h G.M.; observed properties of protestical properties properties of protestical properties of protestical properties of protestical protestical properties of protestical pr	och C.A., Perna r J.D., Rode C.H. H.A., Goeden M. scherichia coli scherichia k., K., Hayashi K., Maktomura K., Nakao, Saito N., Samy J., Takemoto K. region on the l	ALIGNMENTS  RT; 1039 AA.  Q46771;  ence update) tation update) uffing protein).  proteobacteria; Enterobact	HLTR AEEIN AEIN AEIN HLPN HLPN GSSS SMO IG IG SSESX SSESX SESSY TRPY TRPY EIRA
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ane of	land V., G.F., D.J., D.J., Isono K., iki T., ki Y., ki Y.,	iales;	chlamydia t caenorhabdi haemophilus chlamydia p caenorhabdi listeria mo sus scrofa pseudomonas pseudomonas streptococc deinococcus

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Henderson I.R., Meehan M., Owen P.;
Antigen 43, a phase-variable bipartite outer membrane protein,
Antigen 43, a phase-variable bipartite outer membrane protein,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no rest use by non-profit institutions as content modified and this statement is not removed. Usage by ar entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in the genome of Escherichia coli K-12."; Electrophoresis 18:1259-1313(1997).
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SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE CHAIN) ANCHORED TO THE INTEGRAL OUTER MEMBRANE I
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D90838; BAA15825.1; ALT_INIT.
D90839; BAA15832.1; ALT_INIT.
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MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQAN----
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IPR005546; Autotransporter.
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                                                                                              835 LNLVHTS -> MNLIYNA (IN STRAIN ML 3)
847 QGT -> LGA (IN STRAIN ML 3)
855 S -> T (IN STRAIN ML 308-2)
888 Q -> L (IN STRAIN ML 308-2)
1025 S -> I (IN STRAIN ML 308-2)
1025 S -> I (IN STRAIN ML 308-2)
1036 S -> I (IN STRAIN ML 308-2)
1037 S -> I (IN STRAIN ML 308-2)
1038 S -> I (IN STRAIN ML 308-2)
1039 C -> TTT (IN REF. 5).
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K -> N (IN STRAIN ML 308-225).

SL -> FF (IN STRAIN ML 308-225).

T -> K (IN STRAIN ML 308-225).

T -> K (IN STRAIN ML 308-225).

Y -> F (IN STRAIN ML 308-225).

A -> T (IN STRAIN ML 308-225).

B -> V (IN STRAIN ML 308-225).

C -> V (IN STRAIN ML 308-225).

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B -> T (IN STRAIN ML 308-225).

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C -> C (IN STRAIN ML 308-225).
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Pred. No. 5e-0
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No. 5e-05;
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SEQUENCE ENVIRONMENTS / MG1655;
STRAIN=K12 / MG1655;
MEDLINE=71426617; PubMed=9278503;
MEDLINE=71426617; Plunkett G. III, Bloch C.A.,
Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado-Vides J., Glasner J.D., Ro
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MEDLINE-97251357; PubMed-9097039;
Aiba H., Baba T., Fujita K., Hayashi
Kasai H., Kashimoto K., Kimura S., Ki
                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                complete genome sequence complete genome sequence 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       EcoGene; EG11780; ydeK.

PROSITE; PS00013; PROKAR_LIPOPROTEIN;

Hypothetical protein; Membrane; Lipopi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
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MEDLINE-94100243; PubMed-8274505;
Cartwright P.J., Timms M.W., Lithgow T.,
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Nakade
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sl; D90793; BAA15190.1; AL7
3L; D90794; BAA15197.1; AL7
3L; X73395; CAA51730.1; AL7
3; A64905; A64905.
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SIMILARITY:
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             RMKTTTANGQTGQADKFETVTSGTKVTFASGNGTTATVSKDDQGNITVK-YD-VNVGDAL
                                     YQAGSNGQVVVEKGGEWLIKNNDSSIEFQIGNQGTGEATIREGGLYTAENTIIGGNATG-
                                                                  VKIGAKTSVIKEKDGK-LVTGK--
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HYPOTHETICAL LIPOPROTEIN YDEK.

N-ACYL DIGLYCERIDE (POTENTIAL)

N -> K (IN REF. 3).

M -> S (IN REF. 3).
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Pred. No. 0.
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-i- FUNCTION: THIS IS AN ADHESION PROTE ADHERENCE OF DIARRHEA-CAUSING ENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb
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Benz I., Schmidt M.A.;
"AIDA-I, the adhesin involved in diffuse
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Pfam; PF03797; Autotransporter; 1.
Pfam; PF03212; Pertactin; 1.
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the European Bioinformatics Institute
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Similarity

Conservative

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01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein A precursor (190 kDa arantigen) (rOmpA) (rOmp A).
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InterPro; IPR005546; Autotransporter.
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13 X APPROXIMATE TANDEM
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PE II.
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-GTVVFNGGVNGLNVGSN - - VAGTA
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RESULT
YDBA_EC
 Query Match
Best Local
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SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado-Vides J., Glasner J.D., Rc
Plant M., Collado-Vides J., Glasner J.D., Rc
Riley M., Davis N.W., Kirkpatrick H.A., Goe
                                                               EcoGene; EG11
Hypothetical
CONFLICT 4
                                                                                                                                                                                                                                                                   This SWI
                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Sampei G., Seki Y., Siyasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science [2]
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01-FEB-1994 (Rel. 28, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Hypothetical protein ydba.
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                                                                                                                     EMBL;
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"The
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Biochimie 73:1361-1374(1991).
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92190338; PubMed=1665988; Moszer I., Glaser P., Danchin A.; Moszer II., Sinsertion sequences
                                                                                                                                                                          EMBL;
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                                         SEQUENCE
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                                                                                                                                                                                                  e by non-profit institutions as long additied and this statement is not removed. titles requires a license agreement (See send an email to license@isb-sib.ch).
               Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Res. 3:363-377(1996).
                                                                                                                                                                                                                                                      European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                         THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C BETWEEN AMINO ACIDS 839 AND 840.
                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complete genome sequence nce 277:1453-1474(1997).
                                                                                                                 AE000237; AAC74483.1; ALT_SEQ.
AE000237; AAC74487.1; ALT_SEQ.
D90778; BAA15009.1; ALT_SEQ.
D90778; BAA18880.1; ALT_SEQ.
D90779; BAA18881.1; ALT_SEQ.
                                                                                                          X62680;
 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                      replication
                                                                                                                                                                                                              http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                            Usage
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THE GENE CODING
2D/IS30C ELEMENT
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RESULT 6
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                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer pro-
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rO)
(rOmp B) [Contains: 120 kDa surface-exposed protein (Surface)
antigen) (120 kDa outer membrane protein ompB); 32 kDa beta p
                                                   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR-
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIA!
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
                                                                                                                                                                                                                                                                                                                                                OMPB_RICJA
O06653;
                                                                                                                                                                                                   Rickettsiaceae;
                                                                                                                                                                                                                Rickettsia japonica.
Bacteria; Proteobacteria;
                                                                                                       "Sequencing japonica.";
                                                                                                                                   Uchiyama
                                                                                                                                                STRAIN=YH
                                                                                                                                                             SEQUENCE
                                                                                                                                                                                      NCBI_TaxID=35790;
  SUBCELLULAR
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                SIMILARITY)
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PF03797; Autotransporter; 1.
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an email to license@isb-sib.ch).
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3; Mismatches
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32 kDa BETA PEPTIDE.
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    EMBL; AE008659; AAL03623.1; -.
EMBL; AF123721; AAF34129.1; -.
EMBL; AF123726; AAF34129.1; -.
EMBL; AF149110; AAD39533.1; -.
PIR; E97835; E97835.
InterPro; IPR006315; Autotransport.
InterPro; IPR00546; Autotransporter.
Pfam; PF03797; Autotransporter; 1.
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O9KKA3; O9KK98; O9KC45;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence up

28-FEB-2003 (Rel. 41, Last annotation
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                                                                                                                      Pfam; PFO:
TIGRFAMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The rickettsial outer membrane protein A and B genes of Ricke australis, the most divergent rickettsia of the spotted fever submitted (MAY-1999) to the EMBL/Genbank/DDBJ databases -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21442074; PubMed=11557893; Ogata H., Audic S., Renesto-Audiffren Samson D., Roux V., Cossart P., Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Outer membrane protein B precursor (168 kba surface-layer protein) (Surface protein antigen) (Cell surface antigen 5) (Sca5) (Rompb) (Contains: 120 kba surface-exposed protein (Surface protein antigen) (120 kba outer membrane protein ompb); 32 kba beta peptid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=781;
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Rickettsiaceae; Rickettsieae;
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                                                                                                                                                                                                                                                                                                                                ween the Swiss Institute of Bioinf
European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVER LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).
SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
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FUNCTION: THE 32 KDA BETA
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sen the Swiss Institute of Bioinformatics
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requires a license agreement (See
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S-layer; Cell wall; Complete p
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   32 kDa
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120 kDa SURFACE-EXPOSED
32 kDa BETA PEPTIDE.
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30-MAY-2000 (Rel. 39, Created)

30-MAY-2000 (Rel. 39, Last sequence update)

30-MAY-2000 (Rel. 40, Last annotation update)

16-OCT-2001 (Rel. 40, Last annotation update)

Outer membrane protein B precursor (168 kDa surface-layer protein)

(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)

(rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein compB); 32 kDa beta peptide]
                       Rickettsiaceae;
NCBI_TaxID=783;
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                                                                                        Bacteria; Proteobacteria;
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"Cloning, expression and sequence analysis of the gene encoding

"Cloning, expression and sequence analysis of the gene encoding

120 kD surface-exposed protein of Rickettsia rickettsii.";

MOL. Microbiol. 3:1579-1586(1989).

-1- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR

STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL

VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.

-1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED B

LAYER WITH HEXAGONAL SYMMETRY.

-1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
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Hydrolase; Glycosidase; Bacteriolytic enzyme; Cell division; Septation; Repeat; Signal. SIGNAL 1 53 POTENTIAL.
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Bacteria; Firmicutes;
NCBI_TaxID=1351;
                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 299:2071-2074(2003).
-!- FUNCTION: Hydrolyzes the cell wall
M.lysodeikticus. May play an import
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STRAIN=V583 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-91358349; PubMed-1679432; Beliveau C., Potvin C., Trudel J., As "Cloning, sequencing, and expression Streptococcus faecalis autolysin.", Bacteriol. 173:5619-5623(1991).
                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterococcus faecalis."
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MEDLINE=22550857; PubMed=12663927;
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SUBCELLULAR LOCATION:
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SIMILARITY: Contains
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IPR002482; Lysm.
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DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ICE nucleation protein.
GN INAX.
OS Xanthomonac campestris (pv. translucens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; x52970; CAA37140.1; -.
HSSP; P06620; 11NA.
InterPro; IPR000258; Ice_nucleatn.
Pfam; PF00818; Ice_nucleation; 81.
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Mol. Gen. Genet. 223:163-166(1990).
-!- FUNCTION: ICE NUCLEATION PROTEINS ENABLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: OUter membrane (By similarity), DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENS OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE REGIONAL 48 RESIDUE PERIODICITY IS SUPERIMPOSED.
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                                                                                                                                                      AVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAG
                                                                                                                                                                           AGYGSTGTAGADSTLIAGYGSTQTAGSD~~SSLTAGY~~~-GSTQTARQGSDVTAGYGST
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LTAGYGSNSTAGHESSLIAGYGSTQIAGYE
                   IIKGTASGNSRGH-----FGASASVGYQ
                                         STQTAGYNSILTTGYGSTQTAQESSSLTAGYGST--STAGYDSTLTAGYGSTQTAGYKST 1225
                                                                GNARAGIAQAIATA-GLVQAYLPGKSMMAIGGGTYLGEAGY----AIGYSSISAGG--NW
                                                                                      ADSSLIA--GYGSTQTAGYDSNLTAGYGSTQTAREDSSLTAGYGSTSTAGHDSSLIAGYG
                                                                                                          ADAPTLSVDDEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVN
                                                                                                                                                                                                 ADKFETVTSGTKVTFASGNGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSK
                                                                                                                                                                                                                        YGSTGTAGADSTLIAGYGSTQTSGS
                                                                                                                                                                                                                                                                  ----TAGYGSTG-----TAGADSTLIAGYGSTQTSGSDSSLTAGYGSTQTARKGSDMTAG
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Pred. No. 0.
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SG10437; bigA Repeat;

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POTENTIAL.
PUTATIVE SURFACE-EXPOSED VIRULENCE

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REPEATS

(INCOMPLETE).
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101 101 104 114 1123 123 134 145 167 178

252 103 113 122 133 144 155 166 177 188

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STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
McClelland M., Sanderson K.E., Spieth J., Clifton S.W.,
McClelland M., Sanderson K.E., Spieth J., Clifton S.W.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., N
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIGA_SALTY STANDARD; PRT; 1953 AA P25927; P25928; 09XCQ3; 01-MAY-1992 (Rel. 22, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Putative surface-exposed virulence protein
                                                                                     use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                  J. Bacteriol. 173:325-333(1991).
-I- CAUTION: Ref.3 sequence differs in positions 414 and 732.
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                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                   cofactor."
                                                                                                                                                                                                                                                                                                                                                        Wu J.Y., Siegel L.M., Kredich N.M.;
"High-level expression of Escherichia
requirement for a cloned cysG plasmid
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M64606; AAA27042.1;
                           AE008859; AAL22340.1;
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Best Local
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SEQUENCE FROM N.A.
STRAIN=Malish 7;
MEDLINE=94171067; PubMed=8125327;
MEDLINE=94171068 P.A., Weiss K., Walker
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OMPA OR RC1273.
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Rickettsiaceae; Rickettsi
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Raoult D., Fournier P.E., Roux V.;
"Phylogenetic analysis of spotted fever group rickettsiae
of the outer surface protein rompa.";
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ELICITS PROTECTIVE IMMUNITY (BY SIMILARITY)
-!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS CONSTRUCTION: STAYER WITH HEXAGONAL SYMMETRY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Indian tick typhus, M1, Ma
MEDLINE=97015921; PubMed=8862558;
Roux V., Fournier P.E., Raoult D.
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Ogata H., Audic S., Renesto-Audiffren P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence analysis of the 19 conorii (Malish 7 strain)."; Gene 140:115-119(1994).
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Pfam; PF03797; Autotransporter; 1.
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L; A4608674; AAL03811.1; -.
L; U43794; AAB49549.1; -.
L; U43798; AAB49550.1; -.
L; U43806; AAB89551.1; -.
L; U45244; AAB49566.1; -.
L; U46918; AAB49566.1; -.
L; U46918; AAA66663.1; -.
L; U83440; AAC35176.1; -.
L; U83440; AAC35176.1; -.
L; U83448; AAC35184.1; -.
L; U83448; AAC35189.1; -.
L; U83448; AAC35189.1; -.
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J. Biol. Chem. 265:19372-19372(1990).
J. BIOL. Chem. 265:19372-19372(1990).
J. BIOL. Chem. 265:19372-19372(1990).
J. BIOL. Chem. 265:19372-19372.
J. BIOL. Chem. 265:19372-1930.
OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. THIS PROTEIN IS CRITICAL FOR VIRULENCE.
CRITICAL FOR VIRULENCE.
J. SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.
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Campylobacteraceae; Campylobacter.
NCBI_TaxID=196;
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                                                                                                                                                                                                                                                                           EMBL; J05577; AAA23032.1; -. Cell wall; S-layer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERRATUM.
MEDLINE=91035477; PubMed=2229082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=84-32 / 23D;
MEDLINE=90354448; PubMed=2387868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Campylobacter fetus
                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blaser M.J., Gotschlich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Surface array protein of Campylobacter fetus. Cloning and
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1994 (Rel. 29, Last sequence update)
1994 (Rel. 30, Last annotation update)
protein (Surface array protein) (SAP)
                                                                                                                                                                                                                                  Similarity
                    GAKTSVIKEK-----DGKLVTGKGKGENGSSTDEGEG---LVTAKEVIDAVNKAGW
                                                                                                                               DASKSVNV--ETTGTITAFTAAGTGKVDVVAGKISALTADSRTSVNLTATNDTITLTSAN
                                                                                                                                                                             TAITRAALLTDQAELIITKRRTNVENINIISDLETSGDFVFNGYEKVGFNVLGDIVSFAT
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KLNTTAATDQTVTLKANATDNSLEFDSATAKTTSVTASGSGKTLVIKGAEVETLVN----
                                                                                                           TGATTNVTNDNVTD------DEKKRAA-----SVKDVLNAGWNIKGVK
                                                                                                                                                       D-TKGLNFAKETAGT----
                                                                                                                                                                                               SATVKTAVL---ATLLFATVQANATDETGLINVET-----EKLSFGANGKKVNIIS
                                           LATVTLDNAALTAAIDI-----KSASTLNLINSSVNGPKHLYSSKRRYCKFKRAAAKV
                                                              PGTTASDNVDFVRTYDTVEFLSADTKTTTVN-VESKDNG
                                                                                      AATSVNLKQRQAKDATITSAMQQKYNNRRNRIATITSATAVENLTVKHATNVALNGGMDK
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933 AA;
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21.7%;
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Pred. No. 0.07;
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                                                                            Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Elsen J., Heldelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B. DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vanathevan J., Ermolaeva M., White C Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M., "Complete genome sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
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935828; Q46015; Q9RFI2;

01-JUN-1994 (Rel. 29, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAUCR
                         SEQUENCE OF 1-313
STRAIN-ATCC 19089
MEDLINE-89008089;
                                                                                                                                                                                                                                                                                                                                                                                                                   Gilchrist A., Fisher J.A., Smit J.K.;
"Nucleotide sequence analysis of the generous entury stalline surface layer can. J. Microbiol. 38:193-202(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE STRAIN-ATCC 19089 / CB15; MEDIINE-93007489; PubMed-1393820;
              Fisher J
                                                                                                                                                                                                                                                                                "The secretion the C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Alphaproteobacteria;
Caulobacteraceae; Caulobacter.
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Fisher J.A., Smit
Transcriptional
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MEDLINE=21173698; PubMed=
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                                                                                                                                                                                                                                                                H., Awram P.A., Nomellini J.F., Smit J.K.; etion signal of C. crescentus S-layer protein minal 82 amino acids of the molecule."; (OCT-1999) to the EMBL/GenBank/DDBJ databases
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          PubMed=3049545;
J.K., Agabian N
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Cell wall; S-layer; Calo::...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extender by Institute. There are no restruce by non-profit institutions as long as its content
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J. Bacteriol. 170:4706-4713(1988).
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MISCELLANEOUS: THE CALCIUM BINDING OF THIS PROTEIN MAY MEDIATE SURFACE ATTACHMENT BY IONIC BRIDGING BETWEEN THE S-LAYER AND A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA, PROBABLY ACTS AS PHYSICAL BARRIER TO PARASITES AND LYTIC ENZYMES.
SUBCELLULAR LOCATION: CELL WALL, THIS BACTERIUM IS COVERED BY A LAYER WITH HEXAGONAL SYMMETRY. SECRETED BY AN ABC TRANSPORTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,; AF062345; AAC38665.2;
;; AF193063; AAF19365.1;
;; AE005779; AAK22991.1;
A48995; A48995.
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GALTATPTANT-LTLNVNGLTTTGAITDSEAAADDGFTTINIAGSTASSTIASLVAADAT
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1025 AA;
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296989;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein B precursor (168 kba surface-layer protein)
Outer membrane protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
(Surface protein antigen) (Cell surface-exposed protein (Surface protein ompB); 32 kba beta peptide]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Wilmington;
MEDLINE-94040787; PubMed-8224886;
Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;
"Cloning and sequence analysis of the gene encoding the surface layer protein of Rickettsia typhi.";
Gene 133:129-133(1993).
   the European parameters. The surpean parameters is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. However, is a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                      uning W.M., Carl M., Dasch G.A.;
"Mapping of monoclonal antibody binding sites on CNBr fragments the S-layer protein antigens of Rickettsia typhi and Rickettsia prowazekii.";
                                                                                                                                                                                                                                                      membrane protein of rickettsiae: mutant deficient in processing." Infect. Immun. 60:159-165(1992).
                                                                                                                                                                                                                                                                                                                                                                                               MO1
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                                                                                                                                  ant deficient in processing.";
ect. Immun. 60:159-165(1992).
erct. Immun. 60:159-165(1992).
erct. Immun. 60:159-165(1992).
erct. The 120 kba SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTION: THE 120 kba SURFACE-EXPOSED PROTEIN IS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
et al. Color of the following the following and membrane anchor.
ethnotion: The 32 kba beta peptide may serve as a membrane anchor.
ethnotion: The 32 kba beta peptide may serve as a membrane anchor.
ethnotion: Cell Wall. This bacterium is covered by a s-layer with hexagonal symmetry.
ethnotion: Similarity: Belongs to the Rickettsiae ompa/ompb family.
                                                                  European Bioinformatics Institute.
                                                                                SWISS-PROT entry is copyright. It is produced through a en the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                           Immunol.
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requires a license agreement (:an email to license@isb-sib.ch)
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JN0896; JN0896.
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                                                GSVHLTHNTYLITKTINAANQGKIIVAADPINTDTALADGTNLGSAESPLSNIHFATKAA
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1353 120 kDa SURFACE-EXPOSED PROTEIN.
1645 32 kDa BETA PEPTIDE.
1429 MEMBRANE ANCHOR (POTENTIAL).
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V -> I (IN REF. 2)
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G -> S (IN REF. 2)
8 MW; 0CB5641C7EB18
-YANNITTTDANVGSLHFRSGGTSIVSGTVGG
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Search completed: October 6, 2003, 09:23:58 Job time: 10.922 secs

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6: sp_mammal:*
7: sp_mhc:*
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12: sp_virus:*
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   MNKIYRIIWNSALNAWVAVS.....TASGNSRGHFGASASVGYQW
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Copyright (c) 1993 - 2003 Compus
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sp_plant:*
sp_rodent:*
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12.8	12.8	13.8	13.8	13.9	13.9	14.0	14.0	14.3	14.6	15.5	26.4	27.1	33.5	33.6	34.3	36.1	37.1	37.1	85.5	85.5	88.5	88.5	88.5	88.9	88.9	90.1	90.4	92.0
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## ALIGNMENTS

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"Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
EMBL, AF226361; AF42510.1; "Tetters."
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Neisseriaceae; Neisseria.
NCBI_TaxID=487;
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EMBL; AF226376; AAF42525.1; --

EMBL; AF226369; AAF42518 1; --

InterPro; IPR005594; YadA.

Pfam; PE03895; YadA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=NG3/88, and BZ232; MEDLINE=20175756; PubMed=10710308;
                                                                                           Pfam; PF03895;
SEQUENCE 594
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l. 22, La:
n GNA992.
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; Score 2476.5; Pred. No. 2.8e
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Last annotation update)
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Q9JPS2;
Q1-CCT-2000 (TrI
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01-CCT-2002 (TrI
Outer membrane I
GNA992.
                                                                                                      MEDINE-20175756; PubMed-10710308;

Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B
Comanducci M., Jennings G.T., Baldi L., Bartollii E., Capecc
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M.,
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zu
Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Vente
Moxon E.R., Grandi G., Rappuoli R.;
"Identification of Vaccine Candidates Against Serogroup B
                           InterPro;
Pfam; PF03
SEQUENCE
                                                                                                                                                                                                                                                                   Neisseria meningitidis.
Bacteria; Proteobacteria;
Neisseriaceae; Neisseria.
NCBI_TaxID-487;
                                                     Meningococcus by Whole-Genome
Science 287:1816-1820(2000).
EMBL; AF226379; AAF42528.1; -.
InterPro; IPR005594; Yada.
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  Match
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Q9JPR8;
01-OCT-2000 (TrEMBLrel. 15, L:
01-OCT-2000 (TrEMBLrel. 22, L:
01-OCT-2002 (TrEMBLrel. 22, L:
Outer membrane protein GNA992
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Neisseria
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NCBI_TaxID=487;
 SEQUENCE
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X MEDLINE=20175756; PubMed=10710308;

A Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.

A Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecch

A Galectti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., k

A Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuc

A Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin

Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter

A Moxon E.R., Grandi G., Rappuoli R.;

"Identification of Vaccine Candidates Against Serogroup B

Meningococcus by Whole-Genome Sequencing.";

Science 287:1816-1820(2000).
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. 22, Last annotation update)
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E., Capecchi
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                                                                                                                                                                                                                                          O9JPS3, PRELIMINARY; PRT; 590 AA. O9JPS3; O1-OCT-2000 (TrEMBLrel. 15, Created) O1-OCT-2000 (TrEMBLrel. 15, Last sequence up o1-OCT-2002 (TrEMBLrel. 22, Last annotation outer membrane protein GNA992.
   STRAIN=NGE28;
MEDLINE=20175756;
                                                                SEQUENCE FROM
                                                                                                                     Neisseriaceae;
NCBI_TaxID=487;
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Q9JPS0;
Q1-QCT-2000 (TrEMBLrel. 15, Created)
Q1-QCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-QCT-2002 (TrEMBLrel. 22, Last annotation update)
Q1-QCT-2002 (TrEMBLrel. 22, Last annotation update)
Q1-QCT-2002 (TrEMBLrel. 22, Last annotation update)
Q1-QCT-2002 (TrEMBLrel. 32, Last annotation update)
Q1-QCT-2002 (TrEMBLrel. 32, Last annotation update)
Q1-QCT-2002 (TrEMBLrel. 15, Last sequence update)
Q1-QCT-2000 (TrEMBLrel. 15, Last sequence update)
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Q1-QCT-2002 (TrEMBLrel. 15, Last sequence updat
      Neisseriaceae;
NCBI_TaxID=487;
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Science 287:1816-1820(2000).
EMBL; AF226378; AAF42527.1; -.
InterPro; IPR005594; YadA.
Pfam; PF03895; YadA; 1.
SEQUENCE 590 AA; 61661 MW; 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AIGGGTYLGEAGYAIGYSSISAGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                      TNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVNGNARAGIAQAIATAGLVQAYLPGKSMM
                                                                                                                                                                  GSTLTDMLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVR
                                                                                                           NAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPVRI
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Pred. No. 6.2e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20175756; PubMed-10710308;
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
Moxon E.R., Grandi G., Rappuoli R.;
"Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
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SEQUENCE FROM
STRAIN-NGH15;
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Pfam; PF03895; YadA; 1.
SEQUENCE 598 AA; 62763 MW;
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                                                                                                                                                                                                                                               YLPGKSMMAIGGGTYLGEAGYAIGYSSISAGGNWIIKGTASGNSRGHFGASASVGYQW
                                                             DANKPYRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVNGNARAGIAQAIATAGLVQA
                                                                                                             KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSK
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YLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWYIKGTASGNSRGHFGASASVGYQW
                                                DANKPYRITNVAPGYKEGDYTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLAQA
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Science 287:1816-1820(2000).
EMBL; AF226359; AAF42508.1; ..
InterPro; IPR005594; YadA.
Pfam; PF03895; YadA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20175756; PubMed=10710308;
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
Moxon E.R., Grandi G., Rappuoli R.;
"Identification of Vaccine Candidates Against Serogroup B
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2002 (TrEMBLrel. 22,
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NCBI_TaxID=487;
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                                              DANKPYRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVNGNARAGIAQAIATAGLVQA 455
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Pred. No. 1.4e-97;
3; Mismatches 13;
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ dava eMBL; AF157603; AAK68864 l;
Interpro; IPR005594; YadA.
Pfam; PF03895; YadA; 1.
SEQUENCE 598 AA;
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Best Local S
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NCBI_TaxID=487;
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                        YLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGTSASVGYQW
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Pred. No. 3.3e.
5; Mismatches
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annotation
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.3e-97;
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C STRAIN=BZ198, and 297-0;

C STRAIN=BZ198, and 297-0;

X MEDLINE=20175756; PubMed=10710308;

X MEDLINE=20175756; PubMed=10710308;

A Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

A Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.

A Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nutri

A Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.

A Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

A Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.

A Moxon E.R., Grandi G., Rappuoli R.;

T "Identification of Vaccine Candidates Against Serogroup B

T Meningococcus by Whole-Genome Sequencing.";

I Science 287:1816-1820(2000).
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Pfam; PFO;
SEQUENCE
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01-OCT-2000 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TremBLrel.
Outer membrane protein G
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EMBL; AF226358; AAF42507.1; ---
EMBL; AF157604; AAK68865.1; ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings "Identification and characterization of a gene encoding a rmembrane protein of Neisseria meningitidis.";
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Bacteria; Proteobacteria;
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TVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE
                                                                                     SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA
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3895; YadA; 1.
594 AA; 62361 MW;
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83.2%;
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. 15, Last sequence up.
. 22, Last annotation
GNA992 (NhhA outer me
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Pred. No. 4.4e.
3; Mismatches
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O9JPR9,
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20175756; PubMed-10710308;
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti i
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
Ratti G., Santini L., Knapp B., Blair E., Mason T., Tettelin H.,
Broeker M., Hundt E., Knapp B., Blair E., Manoff D.M., Venter C.,
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
Moxon E.R., Grandi G., Rappuoli R.;
"Identification of Vaccine Candidates Against Serogroup B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
EMBL; AF226382; AAF42531.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF03895; Yadi
SEQUENCE 598 AA;
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                                                                                                                                                                           PTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA
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Pred. No. 5.5e
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Best Local S
Matches 493
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A PIZZA M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

A Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,

A Comanducci M., Jennings G.T., Baldi L., Bartolini E., Kuri S.

A Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

A Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

A Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

A Moxon E.R., Grandi G., Rappuoli R.;

"Identification of Vaccine Candidates Against Serogroup B

Meningococcus by Whole-Genome Sequencing.";

Science 287:1816-1820(2000).

R EMBL; ARP26371; AAF42520.1;

R Pfam; PF03895; YadA; 1.
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SEQUENCE
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O1-OCT-2000 (TrEMBLrel. 15, Cro
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O1-OCT-2002 (TrEMBLrel. 22, Las
Outer membrane protein GNA992.
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NCBI_TaxID=487;
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82.0%;
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5; Mismatches
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Last annotation
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Pred. No. 7.76
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Submitted
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"Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
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Neisseria
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GNA992 O
                                                                                                                                                                                               Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B. Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E. Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.; "Complete genome sequence of Neisseria meningitidis serogroup B s
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STRAIN-MC58 / Serogroup B;
MEDLINE-0175755; PubMed=10710307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-MC58 / Serogroup B, BZ169,
MEDLINE-20175756; PubMed-10710308;
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                       Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jenniu
"Identification and characterization of a gene encoding
membrane protein of Neisseria meningitidis.";
                                                                                                                                                                               "Complete genome MC58.";
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                                                                                         SPECIES=N.meningitidis; STRAIN=PMC21;
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01-OCT-2000 (TrEMBLrel. 1:
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Bacteria; Proteobacteria;
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"Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";
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	iers peptide NhhA_deletion_mutar ed mature protein, in claim 12"	n PMC21.	meningococcal disease; meningitis	NhhA deletion mutant #2.			407 AA.	ALIGNMENTS	AAB69136	ABB526//	AAB23859	AAB23856	AAB23854	AAB23857	AAR99394	AAB37832	AAR99393	AAB23860	AAU06181 AAR99392	AAY 23 / 45 AAU06173	AAU06178	AAU06177 AAY23738	AAY23742	AAU06172 AAY27203	AAY23744	AAY23739 AAU06179	AAU06176	AAY23743	AAY57044	AAY23740	AAU06183	AAU06175	AAV23741
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 mutant;
                                           N. meningitidis PMC21 NhhA deletion mutant #3
                                                                        24-OCT-2001
                                                                                                                                   AAU06185 standard;
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                                   GSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADA
                                                                                                              FETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVA
                                                                                                                                            FETVTSGTNVTEASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVA
                                                                                                                                                                                                                                  SVIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADK
                                                                                                                                                                                                                                                             SVIKEKDGKLYTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADK
     GSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label=
52..433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.9%;
94.0%;
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"predicted mature protein, spec
claimed in claim 12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2040; DB 22;
No. 2e-130;
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 Query Match
                                                                            The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhha (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence represents N. meningitidis strain PMC21 surface
                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Peak
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                                                                   antigen
                                                                                                                                                                                                                                                                                    Claim 12;
                                                                                                                                                                                                                                                                                                              New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYQU ) UNIV QUEENSLAND
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igen NhhA deletion mutant
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)B; AAS09176.
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                                                                                                                                                                                                                                                                                  Fig 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    meningitidis
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50..502
/label= Mature_NhhA_deletion_mutant_#4
/note= "Predicted mature protein, spec
claimed in claim 12"
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                                                                                                                                                                                                                                                                                                                                               Surface
mutant;
                                                                                                                                                                                                                                                                                              Neisseria meningitidis strain Synthetic.
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                                                                                                                                                                                                                 Protein
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(UYQU ) UNIV QUEENSLAND
                                25-JAN-2000;
                                                               25-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASAN--
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                                2000US-0177917
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52..512
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ს..51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.1%;
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                                                                                                                                                                mature protein, specifically claim 12"
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                                                                                                                                                                                                                                                                                                                                                                  disease; meningitis
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Matches 407
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                           AAY27202 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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)B; AAS09172.
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                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        407;
                                                                                                                                                                                                                                                                                                                                                                                                     53
                                                                                                                                                                                                                                                                                                                                                                                                                           61
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                                                                                   GTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYS
                                                                                                                                               KGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYS
                                                                                                                                                                                                         ATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQL
                                                                                                                                                                                                                                                                              AGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDA
                                                                                                                                                                                                                                                                                          AGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDA
                                                                                                                                                                                                                                                                                                                            NVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNK
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                                                                                                                                                                                                                                                                                                                                                                             TNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fig 5; 91pp; English.
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                          Protein;
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79.5%;
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Pred. No. 1.2e-127;
0; Mismatches 0; 1
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14-JAN-1998;
01-SEP-1998;
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bacterial
                                                                                                                                                                                                                                                                                                                                                                                                            The invention provides proteins (AAY27201-245) from Neisseria meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167) encoding the proteins. Compositions comprising the protein, nucleic acid or antibody specific to the protein are useful as pharmaceuticals, e.g. a vaccine composition or a diagnostic composition. The composition is also useful for treating or preventing an infection due to Neisserial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New protein and its nucleotide sequence, diagnostic compositions for treating and meningitidis infections
                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 62; 123pp;
                                                                                                                                                                                                                                                                                                                                                                                                   bacteria,
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DB; AAX99124.
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                                                                                  VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
                                                                                                                                                                                                                                                                                          MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASAN-------
SKDDQGNITWMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
                                  GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
                                                                                                                                                                                  NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN
                                                                                                                                                                                                                                YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ
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infection; treatment.
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98GB-0000760.
98GB-0019015.
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68.9%;
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No. 6
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5.6e-125;
hes 0;
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/or preventing Neisseria
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Matches 407
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                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 127-128;
                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis surface meningitidis infections
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DB; AAX85798.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; Protein;
                                                MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL
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                                                                                                                Conservative
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68.9%;
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                                                                                                                0;
                                                                                                           Score 1961; DB 20;
Pred. No. 6.6e-125;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                 meningitidis strain
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              /label= C3
/note= "Conserved :
189..210
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                                                                            /label= V2
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                                                                                                                                                         109..120
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                                                                                                                                                                                                                                                                                                                                           characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhA from N. meningitidis strain PMC21 is 1 of 10 NhhA polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhha (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
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          VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
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VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
                                                 GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
                                                                                                    NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN 180
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Query Match
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Matches 406; Conserv
                                                                                                                                                The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especial in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                            The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis surface proteins useful for treating
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                         Score 1956.5; DB 2
Pred. No. 1.3e-124;
       Mismatches
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                                                                                                                                                                                          infection;
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                                                                                                                                                                                                                       BASB029
                                                                                                                                                                                                                                        21-FEB-2000
                                                                                                                                                                                                                                                                              AAY57045 standard;
 WO9958683-A2
                                                                  Misc-difference
                                                                                                        Misc-difference
                                                                                                                                                                        Neisseria
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                                                                                                                                                                                                                                                                                                                                                               RITHVAPGVKEGDVTHVAQLKGVAQNLHNRIDHVDGHARAGIAQAIATAGLVQAYLPGKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QNGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASAN------
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||KIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANNERPRKKD
                                                                                                                                                                                                                                                                                                                                                                                                              VNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVD
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                                                                                                                                                                                                                                                                                                                                                                                                    VNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV
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                                                                                                                                                                        meningitidis
                                                                                                                                                                                        treatment;
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                             /note=
389
                                                /note=
269
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123
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98
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92
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                                                                                                                                                                                                   HSF; diagnosis;
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Best Local
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                                                                                                                                                                                                                                                                                                        Sequence
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DB; AAZ39865.
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361
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                                                                                                                                                                                                                                        1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASAN-------
                                                                                                                                                                                                                                                                            Similarity
GIGSTLIDTLLNIGATINVINDNVIDDEKKRAASVKDVLNAGWNIKGVKPGITASDNVDF
                                     TDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
                                              TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
                                                                           VRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
                                                                                    VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
                                                                                                                                                     NGSNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN 180
                                                                                                                                                                                        YLDPVQRTVAVLIVNSDKEGTGEKEKVEEDSNWAVYFDEKGVLTAREITLKAGDNLKIKQ
                                                                                                                                                                                                                              MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL
                                                                                                                                                                                                                                                                                                                          the protein.
                                                                                                                                                                                                                                                                                                        591 AA;
                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                           94.78;
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                                                                                                                                                                                                                                                                  Score 1954; I
Pred. No. 2e-1
1; Mismatches
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DB 21; 1;

591; 184;

Indels Length

Gaps

52 60

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52

52

-NVDF 56

240

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This is the Nisseria meningitidis BASB029 amino acid sequence from CC serogroup B strain H44/76. The BASB029 protein is homologous to the Haemophilus influenzae surface fibril (HSF) protein. The invention CC relates to BASB029 polynucleotide sequences (AAX39864-Z3985) and Dolypeptide sequences (AAY57044-Y57045) and their immunogenic fragments. CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria CC meningitidis infection in a mammal. Compositions containing BASB029 polypeptides are useful for generating an immune cresponse in an animal. A therapeutic composition comprising an antibody CC directed against BASB029 is useful in treating humans with Neisseria CC meningitidis disease. The polynucleotide is useful in the diagnosis of the stage of infection, type of infection, susceptibility to an CC the stage of infection, type of infection, susceptibility to an CC infection which results from increased or decreased expression of the CC polynucleotide, and for therapeutic or prophylactic purposes, CC polynucleotides and polypeptides are also useful in the CC particularly bacterial infections. The protein is useful in the CC particularly bacterial infections. The protein is useful in the CC portein is useful for the stimulation of the immune system of an organism or protein is useful for the stimulation of the immune system of an organism or protein is useful in the stimulation of the immune system of an organism or protein is useful in the stimulation of the immune system of an organism or protein is useful in the stimulation of the immune system of an organism protein is useful in the stimulation of the immune system of an organism protein is useful in the stimulation of the immune system of an organism protein is useful in the stimulation of the immune system of an organism protein is useful in the stimulation of the immune system of an organism protein is useful in the stimulation of the immune system of an organism protein is useful in the stimulation of the immune system of an organism protei
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                                                   system of an organism
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236

360 176 116 240 56

300

420

480

296

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ARESULT 10
ARY23741
ID ARY23
XX ARY23
XX ARY23
XX O8-SE
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Best Local Similarity
Matches 405; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A surface protein of Neisseria
                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                  The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especial in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans the detection or diagnosis of N. meningitidis infection in humans the detection or diagnosis of N. meningitidis infection in humans the detection or diagnosis of N. meningitidis infection in humans the detection or diagnosis of N. meningitidis infection in humans the detection or diagnosis of N. meningitidis infection in humans the detection of diagnosis of N. meningitidis infection in humans the detection of diagnosis of N. meningitidis infection in humans the detection of diagnosis of N. meningitidis infection in humans the detection of diagnosis of N. meningitidis infection in humans the detection of diagnosis of N. meningitidis infection in humans the detection of diagnosis of N. meningitidis infection in humans the detection of diagnosis of N. meningitidis infection in humans the detection of diagnosis of N. meningitidis infection in humans the detection of diagnosis of N. meningitidis infection in humans the detection of diagnosis of N. meningitidis infection in humans the detection of diagnosis of N. meningitidis infection in humans the detection of diagnosis of N. meningitidis infection in humans the detection of diagnosis of N. meningitidis infection in humans the detection of diagnosis of N. meningitidis infection in humans the detection of diagnosis of N. meningitidis infection in humans the detection of diagnosis of N. meningitidis infection in humans the detection of diagnosis of N. meningitidis infection in humans the detection of diagnosis of N. meningitidis infection in humans the detection of diagnosis of N. meningitidis infection in humans the detection of diagnosis of N. meningitidis infection in humans the detection of diagnosis of N. meningitidis infection in humans the det
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Surface protein; surface glycoprotein; infection; vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 104-106; 132pp; English.
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YLDPVLRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ
                                                                                                             MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASAN----
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                                                                                     MNEILRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL
                                                                                                                                                                                                                                                                         591 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GIGSTLIDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
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                                                                                                          /label= V3
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Best Local
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                                                                                                                                                                                                                                                                                                                                                     MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASAN------
              SKDDQGNITYMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
                                                                                                                             VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
                                                                                                                                                                                                                           NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN
                                                                                                                                                                                                                                                                                 YLDPVLRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ
                                                                      TDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETYTSGTNYTFASGKGTTATV
                                                                                                                                                                                                                                                                                                                                        MNEILRIIWNSALNAWYVVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL
SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
                                                       TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
                                                                                                            VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
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                              The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhhA (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence represents N. meningitidis strain H41 surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Surface mutant;
                                                                                                                                                                                              New NhhA surface antigen polypeptides and polynucleotides Neisseria meningitidis, useful in producing vaccines for t preventing broad spectrum of Neisseria meningitidis -
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                                                                                                                                                                        Claim 12; Fig 6; 91pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           meningitidis strain
                                                                                                                                                                                                                                                                              Jennings
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                                                                                                                                                                                                                                                                                                      QUEENSLAND
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52..513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H41 NhhA deletion mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NhhA;
                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             meningococcal disease; meningitis vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal_peptide
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                                                                                                                                                                                                            treating
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Sequence

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RESULT 13
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Best Local Similarity
Matches 393; Conserv
                                                                                                                                                                                                                                                                     N. meningitidis
  Region
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                                                                                                                                                                                             Key
                                                                                                                                                                                                                      Neisseria
                                                                                                                                                                                                                                              Surface
                                                                                                                                                                                                                                                                                           24-OCT-2001
                                                                                                                                                                                                                                                                                                                    AAU06180;
                                                                                                                                                                                                                                                                                                                                          AAU06180 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Н
                                                                                                                                                                                                                                             antigen NhhA; meningococcal disease; meningitis vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSKKDNKPVRIINVAPGVKEGDVTNVAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NVESKDNGKKTEVKIGAKTSVIKEKDGKLYTGKDKGENGSSTDEGEGLYTAKEVIDAVNK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASA------
                                                                                                                                                                                                                                                                                                                                                                                                     SSISAGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                                                                                                                                                                                                                                                                                                                 SSISDGGNWIIKGTASGNSRGHFGASASVGYQW 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDMLLNTGATTNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDETGLINV
                                                                                                                                                                                                                     meningitidis strain Z2491
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                                                                                                                                                                                                                                                                                          (first entry)
                                                                        /label= C2
/note= "Conserved
115..124
  /label= C3
/note= "Conserved
189..208
                                                                                                                                                /note= "Conserved region 51..102
                                                                                                                                                                                                                                                                     Z2491
                                    /note= "Variable
125..188
                                                                                                              103..114
                                                                                                                                   /label= V1
                                                             /label=
                                                                                                                                                                                            Location/Qualifiers
                                                                                                                       /note= "Variable region 1"
                                                                                                                                                                      /label=
                                                                                                                                                                                                                                                                                                                                          Protein;
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                                                                                                                                                                                                                                                                     surface
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Pred. No. 1.9e
4; Mismatches
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                                                                                                                                                                                                                                                                   antigen NhhA polypeptide sequence.
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L.9e-121;
nes 10;
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                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                        meningitidis mutant polypeptides of the surface antigen NhhA (AAU06182-AAU06186). The modified or mutant NihA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain Z2491 is 1 of 10 NhhA polypeptide sequences (AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-488774/53
N-PSDB; AAS09170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peak
                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Fig 1; 91pp; English.
                                                                                                                                                                                                                                                                                                                  the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to the isolation of novel Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYQU ) UNIV QUEENSLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JAN-2000; 2000US-0177917
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  241
                                               181
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                                                                        52
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                                                                                                                                             61
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                                                                                                                                                                                                                                                       Similarity
VRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGKGENGSS
                                                                                                                                                                                                          MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLEATVQASA-------
                         VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
                                                GIGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNIKGVKTGSTTGQSENVDF
                                                                                               NASSFTYSLKKDLTGLINVETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN
                                                                                                                                               ESVQRSVVGSIQASMEGSGELETISLSMTNDSKEFVDPYIVVTLKAGDNLKIKQNTNENT
                                                                                                                                                                                             MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jennings
                                                                                                                                                                                                                                                                                           592
                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                           AA;
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/note= "Variable r
237..592
/label= C5
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/note= "Variable region
209..227
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                                                                                                                                                                                                                                           Score 1893.5;
Pred. No. 2.5e
4; Mismatches
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2.5e-120;
les 7;
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                                                                                                                                                                                                                                                                  22;
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RESULT 14
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 Best Loca
Matches
                     Query Match
                                                         The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                  Claim
                                                                                                                                                                                     Neisseria meningitidis surface meningitidis infections
                                                                                                                                                                                                                                                                                                                                                                                                                    Surface
                                                                                                                                                                                                                                                                                                                                                                                                                                       A surface
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY23740 standard;
                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                  Jennings MP,
                                                                                                                                                                                                                                                                                                      12-DEC-1997;
                                                                                                                                                                                                                                                                                                                         14-DEC-1998;
                                                                                                                                                                                                                                                                                                                                             24-JUN-1999.
                                                                                                                                                                                                                                                                                                                                                                  W09931132-A1
                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                        Surface protein; surface immunoreactive peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY23740;
                                          Sequence
                                                                                                                                                                                                                                                                      OYQU)
                                                                                                                                                                                                                                                                                 (ISIS-)
 Local Similarity
nes 395; Conserv
                                                                                                                                                                                                                     1999-418754/35
DB; AAX85792.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301
                                                                                                                                                                  1; Page 100-101; 132pp;
                                                                                                                                                                                                                                                                      VIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASYGYQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NINAGNNIEISRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSKKDNKPV
                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                         594 AA;
  Conservative
                                                                                                                                                                                                                                                                      INNOVATION QUEENSLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                 Moxon
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                                                                                                                                                                                                                                                                                                                         98WO-AU01031
                                                                                                                                                                                                                                                                                                                                                                                                                                     of Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                  ER,
         91.5%;
                                                                                                                                                                                                                                                                                LTD
                                                                                                                                                                                                                                                                                                                                                                                                                 glycoprotein;
                                                                                                                                                                                                                                           Peak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    594
Score 1887.5; DB 2
Pred. No. 6.4e-120;
5; Mismatches 7;
                                                                                                                                                                                                                                                  IRA;
                                                                                                                                                                  English.
                                                                                                                                                                                                proteins useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                   infection;
                   20;
                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine;
 Indels
                                                                                                                                                                                               treating
                   Length 594;
 187;
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RRESULT 1:
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ID AAX'S7044
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CC This is the Nisseria meningitidis BASB029 amino acid sequence from CC serogroup B strain ATCC13090. The BASB029 protein is homologous to the CC Haemophilus influenzae surface fibril (HSF) protein. The invention CC relates to BASB029 polynucleotide sequences (AAZ3964-Z39865) and CC polypeptide sequences (AAX57044-Y57045) and their immunogenic fragments CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria CC meningitidis infection in a mammal. Compositions containing BASB029 polynucleotides and polypeptides are useful for generating an immune CC response in an animal. A therapeutic composition comprising an antibody CC directed against BASB029 is useful in treating humans with Neisseria CC the stage of infection, type of infection, susceptibility to an CC infection which results from increased or decreased expression of the Stage of infection and for therapeutic or prophylactic purposes, particularly genetic immunisation. Antibodies against BASB029 CC polynucleotides and polypeptides are also useful for treating infections CC particularly bacterial infections. The protein is useful in the Screening and development of antibacterial drugs. Fused recombinant constants and constants are also useful for treating infections. Query Match Best Local S Matches 395 New Sequence Claim 4; Fig 2; 74pp; English. treatment protein is useful for the stimulation of the immune system of an organism polypeptide from neisseria meningitidis useful for diagnosis, atment or prevention of bacterial infections in mammal 354 481 294 421 235 361 175 301 2000-053103/04. 241 181 121 55 51 395; 51 61 51 Similarity KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHEGASASVGYQW TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSKKDNK 293 TVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE SSTDEGEGI.VTAKEVIDAVNKAGWRWKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA DFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENG 114 LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV NTNASSFTYSLKKDLTDLTSVGTEKLSFSANSNKVNITSDTKGLNFAKKTAETNGDTTVH 180 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQAS------TVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE SSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA DFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKDKGEND PVQRTAVVLSFRSDKEGTGEKEVTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE 120 the 594 AA; Conservative protein. 91.5%; Score 1887.5; DB 21; Length 594; Pred. No. 6.4e-120; 5; Mismatches 7; Indels 187; -----ANNV Gaps 174 300 240 234 54 360 50 50 60 50 2

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APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
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US-08-913-942-15
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US-08-868-347-26
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Pred. No. 1e-155;
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APPLICANT: DENKINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
FRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR PERIOR TON NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
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Patent No. 6333173
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                                                                  VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS 116
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TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
                                                                                                          GIGSTLTDTLLNTGATTNYTNDNYTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
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Pred. No. 1e-155;
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US-09-377-155-2
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LENGTH: 592
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Best Local Similarity
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APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE
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CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
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VSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDET
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CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
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                  VNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV
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US-09-377-155-11
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CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEO ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
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JENNINGS, Michael Paul
MOXON, E. Richard
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ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM
                                                            NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR 296
                                                                                                     SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
                                                                                                                   SKDDQGNITWMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV 236
                                                                                                                                                              TDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
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                                                                                                                                                                                                                                                                                 GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
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Pred. No. 1e-154;
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CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GE 9726398.2
PRIOR APPLICATION NUMBER: GE 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER: OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 11
LENGTH: 591
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Matches 395;
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APPLICANT: MOXON, E
TITLE OF INVENTION:
FILE REFERENCE: 065
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CURRENT FILING DATE: 1990-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
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No. 619731
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JENNINGS, Michael Paul
MOXON, E. Richard
MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQAS-------
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CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
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Best Local Similarity
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KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 407
                                                             PVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPG
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Pred. No. 1.4e-149;
5; Mismatches 7; Indels 187;
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RESULT

RESULT 10
US-09-669-974-15
; Sequence 15, Application U
; Patent No. 6333173
; GENERAL INFORMATION:

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Sequence 15, Application US/0937;
patent No. 6197312
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard AI
APPLICANT: JENNINGS, Michael PR
APPLICANT: MOXON, E. Richard
APPLICANT: MOXON, E. RICHARD
APPLICANTINENTION: NOVEL SURFF
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; TYPE: PRT
; ORGANISM: Neisseria meningitidis
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SEQ ID NO 15
FENGTH: 599
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Best Local S
Matches 396
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CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
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            AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
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AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                        KDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQ
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Pred. No. 2e-1
3; Mismatches
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RESULT 11
US-09-377-155-7
; Sequence 7, Application U
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Ri
; APPLICANT: JENNINGS, Mi
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APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
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TYPE: PRT
ORGANISM: Neisseria meningitidis
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Pred. No. 2e-1
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Sequence 7, Application US/09669974
Patent No. 6333173
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SUFFACE ANT)
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/6699
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APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: US/09/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 594
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DFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENG
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                                            PVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPG
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SURFACE ANTIGEN US/09/669,974

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US-09-377-155-17
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PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR PPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
                                                                                                      Sequence 17, Application US/09377155 Patent No. 6197312 GENERAL INFORMATION:
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Best Local Similarity
Matches 395; Conserv
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              APPLICANT: PEAK, Ian Richard Anselm APPLICANT: JENNINGS, Michael Paul APPLICANT: MOXON, E. Richard TITLE OF INVENTION: NOVEL SURFACE ANTIGEN FILE REFERENCE: 065064/0128 CURRENT EPILICATION NUMBER: US/09/377,155 CURRENT FILING DATE: 1999-08-19
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TYPE: PRT
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ilarity 66.5%;
Conservative
                                                      SURFACE ANTIGEN
    PCT/AU98/01031
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Pred. No. 6.7e-149;
3; Mismatches 9;
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; TYPE: PRT
; ORGANISM: Neisseria
US-09-377-155-17
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PRIOR APPLICATION NUMBER: GB 9
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                     Sequence 17, Application US/09669974 Patent No. 6333173
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Best Local Similarity
                                                              APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-9-26
CURRENT FILING DATE: 2000-9-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
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Pred. No. 4.6
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MMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHEGASASVGYQW
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION. NOVEL SURFACE.ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR APPLICATION UMBER: GB 9726398.2
PRIOR APPLICATION SUMBER: GB 9726398.2
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; ORGANISM: Neisseria
US-09-669-974-17
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US-09-377-155-13
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NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
LENGTH: 592
TYPE: . THE SECOND SEQ ID NO 17
                                                                                                                                                                                                                                    Sequence 13, Application US/09377155 Patent No. 6197312 GENERAL INFORMATION:
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Pred. No. 4.6e-148;
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; LENGTH: 598
; TYPE: PRT
; ORGANISM: Nei
US-09-377-155-13
Search completed:
Job time: 13.884
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd

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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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AGSSGKVISGNVSPSKGKMDETV 236	KEETVISGINVIFASGKGITATV 176 	rsvikekDgklvTgkDkGengss 116 	VLNAGWNIKGVKPGTTASDNVDF 240	OTKGLNFAKETAGTNGDTTVHLN 180	52	NEKGVLTAREITLKAGDNLKIKQ 120	52	/LATLLFATVQASAN 52                 /LATLLFATVQASANNEEQEEDL 60	; Length 591; 2; D; Indels 184; Gaps 1;	(strain MC58 serogroup B)  #text_change 19-Jan-2001  fries, A.C.; Nelson, K.E.; Eisen, Fleischmann, R.D.; Dougherty, B. V.; Masignani, V.; Pizza, M. C.M.; Moxon, E.R.; Rappuoli, R.; gittidis serogroup B strain MC58. 10307

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A; Residues: 1-592 <PAR>
A; Cross-references: GB:AL162755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A81775; MUID:20222556; PMID:10761919 A; Accession: A81888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Parkhill, J.; Achtman, M.; James, Holroyd, S.; Jagels, K.; Leather, Nature 404, 502-506, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable surface fibril protein NMA1200 [imported] - C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #t C;Accession: A81888
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Best Local S
Matches 396
                   296
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                                                                                                                             RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKS
                                                                                                                                                                                                                               TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
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                                                                       NINAGNNIEITRNGKNIDIATSMTPQFSSYSLGAGADAPTLSVDGD-ALNVGSKKDNKPV
                                                                                                                                                                                                             TDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
                                                                                                                                                                                                                                                                                                                                                                GIGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNIKGVKTGSTTGQSENVDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASA-------
                                                     NINAGNNIEISRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPV
                                                                                                                                                                                                                                                                                                                                                                                                                                          NASSFTYSLKKDLTGLINVETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN
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Pred. No. 3.1
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S.; Moule, S.;
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7;
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Mungall, K.; Quail, M.A.;
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Rajandream,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer as Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
R,Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A.Y.; Martino; C.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
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A82615
Surface protein XF1981 [imported] - xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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                                                                                                                                                                       В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; anonymous, The Xylella Nature 406, 151-157, 2000
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A; Contents: annotation
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               VTSSGINAG-----SQKITNVAAGTADTDAVNLSQLNTAMAGSGAKSVHYYSTYD----
                                                                                                                                                                                                           GNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSV-----DGDALNVGSK-----KD
                                                                                                                                                                                                                                               ADAKEAT -- DAVNLRQLDRVAQDANRYVDNKIESLSEGQTF----
                                                                                                                                                                                                                                                                       TVMYDVNVGDALNVNQL---
                                                                                                                                                                                                                                                                                                                           ASADGSVALGD-GAKDGARGAESYTGKYSGLQNNTVGTVSVGDASKGETRTVS-----NV
                                                                                                                                                                                                                                                                                                                                                              TAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNI
                                                                                                                                                                                                                                                                                                                                                                                                                                          LSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENG-SSTDEGEGLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IWNSALNAWVVVSELTRNHTKRASATVKT-AV-LATLLFATVQASANNVDFVRTYDTVEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 407
                                                                                                                                                                                                                                                                                                                                                                                                    --GGTQGGNYNGDGATGTRSIAVGVGTLASA---
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                                                                                           NAVAIGNHSVADRANTVSVGSAGSERQVTNVAAGTADTDAVNVSQLNQGLITAKQYTDGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                       -----SATP----IAAGVDATAIGVGATASGADSIAMGNKASASAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.5%; Score 341; DB 2; 27.4%; Pred. No. 1.9e-11;
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                                                                                                                                                                                                                                                                                   -QNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                               -RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161;
                                                                                                                                                                                                                                                                                                                                                                                                    - EGATAVGSGAAASGKGSTAIGRNAV
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Gaps

GSPDB:GN

1008 240 964 184 124

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A;Cross references: GB:AE003982; GB:AE003849; NID:g9106554; PIDN:AAF84338.1; GSPDB:GN001 A;Experimental source: strain 9a5c R:Simpson, A.J.G.; Reinacch, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Abriones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, Bas Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000

A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigi Chado, M.A.; Madeira, M.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Marrins, E.A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.A.; de Sa, R.G.; Santelli, R.V.; Savassak A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, A.M.; Verjovski-Almeida, S.; Vettore, A.L.; Z. A.B.; Santelli, R.V.; Savassak A; Authors: da Silva, A.M.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z. A.B.; Santelli, R.V.; Savassak A; Althors: da Silva, A.C.R.; da Silva, R.G.; Santelli, R.V.; Savassak A; Althors: da Silva, A.C.R.; da Silva, R.G.; Vettore, A.L.; Z. A.B.; Santelli, R.V.; Savassak A; Althors: da Silva, R.G.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z. A.B.; Santelli, R.V.; Savassak A; Althors: da Silva, R.G.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z. A.B.; Santelli, R.V.; Savassak A; Althors: da Silva, R.G.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z. A.B.; Savassak A; Althors: da Silva, R.G.; Vettore, A.L.; Z. A.B.; Savassak A; Althors: da Silva, R.G.; Vettore, A.L.; Z. A.B.; Savassak A; Althors: da Silva, R.G.; Vettore, A.L.; Z. A.B.; Vettore, A.L.; Z. A.B.; Vettore, A.L.; Z. A.B.; Vett
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D82671
probable adhesin Z5029 [imported] - Escherichia coli (strain O157:H7,
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep
                                                                                                   RESULT
A86036
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Similarity 29.3%; Pred. No. 1.1e-10;
98; Conservative 53; Mismatches 112;
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A; Dialus, France, DNA
A; Molecule type: DNA
A; Residues: 1-1588 <HAY>
A; Cross-references: GB:BA000007; PIDN:BAB37903.1; PID:g13363955; GSPDB:GN00154
- Proprimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                              gasawara, N.; Yasunaga, T.; Kuhara, S.; SHLUM, L., L., DNA Res. 8, 11-22, 2001

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia
A;Title: Complete genome sequence of enterohemorrhagic Escherichia
                                                                                                                                                                                                                                                                                    probable adhesin ECs4480 [similarity] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli (c;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Nov-2001 C;Date: 18-Jul-188 C;Accession: H91188 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
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A;Residues: 1-1588 <STO>
A;Cross-references: GB:AE005174; NID:g12518349; PIDN:AAG58749.1; GSPDB:GN00145; UWGP:A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z5029
A; Experimental source: C; Genetics: A; Gene: ECs4480
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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Nature 409, 529-533, 2001
                                                                                                                                                                                   A; Reference number: A99629; A; Accession: H91188
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DEVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVI 9	Nature 413, 848-852, 2001 A; Authors: Parry, C.; Quall, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Allthors: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A; Reference number: AB0502; MUID:21534947; PMID:11677608 A; Reference number: AB0502; MUID:21534947; PMID:11677608 A; Residues: AC0976 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-1107 < PAR> A; Cross - references: GB:AL513382; PIDN:CAD03303.1; PID:g16504923; GSPDB:GN00176 C; Genetics: A; Gene: sapB Query Match Best Local Similarity 26.7%; Pred. No. 2.6e-10; Matches 115; Conservative 59; Mismatches 176; Indels 80; Gaps 15;	Qy 392 NSRGHPGASASVGYQW 407	1337 SRVTNIENGIGDIVTTGSTKYFKTNTDGVDASAQGKDSVAIGSGSIAAADNSVALGTGSV 233DETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD 234DETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD 235DETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD 236	Best Local Similarity 26.8%; Pred. No. 9.7e-11;  Matches 117; Conservative 59; Mismatches 168; Indels 92; Gaps 15;  Qy 46 TVQASANNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEK 100    :
231 KMDETVNINAGNNI-EITRNGKNIDIATSMTPQ	Qy  3 KIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANNVDFV 57	{D	398 GASASVGYQW 407  :   1098 SAAIGAGFQW 1107	Qy  192VGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVN 237  862 ENGIGDIVTTGSTKYFKINTDGADANAQGADSVAIGSGSIAAAENSVALGINSVADEANT 921  Qy  238 INAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDGDALNVGS 288  ::  ::

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surface-exposed outer membrane protein XF1516 [imported] - Xylella fastidiosa C; Species: Xylella fastidiosa C; Species: Xylella fastidiosa C; Date: 18 Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C; Accession: C82672 R; Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleot Nature 406, 151-157, 2000 A; Title: The genome sequence of the plant pathogen Xylella fastidiosa. A; Reference number: A82515; MUID:20365717; PMID:10910347 A; Note: for a complete list of authors see reference number A59328 below A; Accession: C82672 A; Status: preliminary A; Molecule type: DNA Crus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adhesin homolog HI1732 - Haemophilus influenzae (strain Rd KW20)
C. Species: Haemophilus influenzae
C.Date: 1BeAug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Oct-1997
C. Accession: I64138
R.D.: Adams, M.D.: White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Fleischmann, R.D.: Adams, M.D.: White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.: Scott, J.: Shirley, R.: Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M., Science 269, 496-512, 1995
A.;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A.;Reference number: A64000; MUID:95350630; PMID:7542800
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C82672
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A;Residues: 1-298 <TIGR>
A;Cross-references: GB:U32846; GB:L42023; NID:g1574588; PID:g1574589;
A;Residues: Ī-1004 <SIM>
A;Cross·references: GB:AE003981; GB:AE003849;
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.;
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPKTSVIKDNNGKLLTGKQLKDANT----
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    A.A.;
                           P.; Abreu, F.A.; Acencio, M.; Alvarenga,
                                                                     NID:g9106543;
    Camargo,
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    L.E.A.;
                                                                     PIDN: AAF84325.1;
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    Carraro,
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A; Authors: Ferreira, V.C.A.; Emper, E.L.; Kitajina, J.P.; Krieger, J.E.; Kuramae, E.E.; La Junqueira, M.L.; Kemper, E.L.; Kitajina, J.P.; Krieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A; Muthors: Martins, E.M.F.; Matsukuma, A; M. Menck, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa, A.Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, F.R.; da Silva, A.M.; Silva, Jr., W.A.; da Silva, A.G.R.; Verjovski-Almeida, S.; Vettore, A.L., Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Contents: annotation C; Genetics:
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                                                                                                                           401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAVLAT - - - LLFATVQASAN - NVDFVRTYDTVE - - - - - - - -
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LGG----QSTAISEGGTSLGYNSFVGQSATNG
                                                           DGGNWIIKGTA---SGNSRGH---FGASASVG
                                                                                                                                                                                       ---DGNARAGIAQAIATAGLVQAYLPGKSMMAIG-----
                                                                                                                                                                                                                                                                                                                                                                                    GQGGVSLGYNSFVGEGSFNGLALGSNSLVLLQGVD-----SVALGSGSMASEPNV
                                                                                                                                                                                                                                                                                                                                                                                                                                      SKGKMDETVNINAG----NNIEITRNG----KNIDIATSMTPQFSSVSLGAGADAPTLSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKESTAIGSGAQAVADNTVAF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GKGTTATVS-KDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FAPNA-IALGYNSSVTQSANNGVALGSNSTVSGVNSVALGAGSMASELNVISVGGGDGVT 182
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                                                                                                                       TQTTGSGVASVSGQDSTAAGASAQAAGDSSTALGARSRANAIGSSALGVDGHALGANSTA
                                                                                                                                                                                                                                                                                                                  ----DGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --DAVNKAGWRMKTTTANGQTGQADKFETV----TSGTNVTFAS 168
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488
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R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre, Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                          probable autotransporter protein yapH [C;Species: Yersinia pestis C;Date: 02-Nov-2001 #sequence_revision C;Accession: AD0123
                                                                                                              Nature 413, 523-527, 2001
A;Title: Genome sequence of
A;Reference number: AB0001;
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3705 <KI
A;Cross-references: GI
                                                                                             A; Accession: AD0123
                        <KUR>
  GB:AL590842;
                                                                                                                   of Yersinia pestis,
01; MUID:21470413; P
  PIDN:CAC89847.1;
                                                                                                                                                                                                                                                                                                                                 [imported] -
                                                                                                                                                                                                                                                                                        02-Nov-2001
                                                                                                                     PMID:11586360
                                                                                                                                            the
  PID:g15979073;
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                                                                                                                                                                                                                                                                                                                                    Yersinia pestis (strain
                                                                                                                                         agent of
  GSPDB:GN00175
                                                                                                                                            plague
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Barrel

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RESULT 12
S28634
     A; Experimental source: strain 2787 R; Suhr, M.; Benz, I.; Schmidt, M.A Mol. Microbiol. 22, 31-42, 1996
                                                                                                                                                                                                       MOl. Microbiol. 6, 1539-1546, 1992
A;Title: AIDA-I, the adhesin involved in d.
A;Reference number: S22680; MUID:92326638;
A;Accession: S22680
                                                                                                                                                                                                                                                                                                                                                                                                        adhesin AIDA-I precursor - Escherichia coli plasmid
c;Specites: Escherichia coli
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993
C;Accession: S28634; S22680; S28881; S72657
R;Benz, I.
                                                                                               A;Cross-references: EMBL:X65022
A;Experimental source: strain 2
A;Accession: S28881
                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-1286 <BEN>
A; Cross-references: EMBL: X65022; NID: g42254; PIDN: CAA46156.1;
R; Benz, I.; Schmidt, M.A.
                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data A; Reference number: $28634 A; Accession: $28634
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                                                              A; Molecule type: protein A; Residues: 50-56 <BE3>
                                                                                                                                                    A; Molecule type: DNA
A; Residues: 839-1286 <BE2>
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A; Gene: yapH
                                                                                                                                                                                        A;Status: nucleic acid sequence not
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Benz, +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KATNTGILATKNANNASDIYIRSAGDITAATGISATHNGTGTVKIKNDGTITSTTAGIAI 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIDIATSMTPQF-----SSVSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LT---VNMTSNQVVIDGQGKFGLTVNNTTNYGL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KIVLQSRSDGSIIS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K------EGDVTNVAQLKGVAQNLNNRIDNVDGNARAGI-AQAIATAGLVQAYLPGKSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGDLTSTGVNAFAYTFADGASFELIANQNVFSGTTTNRGLEIGSYNS----IDGFGSGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVNDRAQEIGEVNKLAFTGRFHVTHTGSSVTSFVSTGGANNTSTMDFASGADVKIDRTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -VNQLQNSGWNLDSKAVAG-----SSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MSKIDSANYYSMVVLNGANTAVNVIYNNIDFLGSSQLIYMGAYGAATNSIMTFGDILNDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLGSIVFLS-----TGPVFAADITVSTQAELSAALS----NGTYDKIILGADITLIGS
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                                                                                                                                                                                                                                                                                                                                                                                       Library,
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                                                                                                                                                                                                                                          involved in diffuse adherence of
                                                                                                                    2787
                          M.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 188.5;
Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                         March 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RGEAGYAIGYSSISDG-GNWIIK--GTASGNSRGHFG
                                                                                                                                                                                                                             PMID: 1625582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .023;
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RESULT 13
AB3486
C; Species: Brucella melitensis
C; Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C; Date: 01-Feb-3002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C; Accession: AB3486
R; DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghar Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A; Title: The genome sequence of the facultative intracellular pathogen Bruce
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A; Residues: 1-365 < KUR>
                                                                                                                                                                                                                               A;Reference number: AD3252; PMID:11756688 A;Accession: AB3486
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F;50-1286/Product:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein A; Residues: 847-856 <SUH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Processing of the AIDA-I precursor: removal of A;Reference number: S72657; MUID:97055419; PMID:8899706 A;Accession: S72657
                                                                                                    A; Gene:
                                                                                                                                      A; Experimental source:
                                                                                                                                                            A; Cross-references:
                                                                                                                                                                                                                  A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Genome: plasmid pIB6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Keywords: membrane protein;1-49/Domain: signal sequence
                                            Query Match
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GY 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STSVYNSGVQTVFAGATVTDTTVNSGGNQNISS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I -- STHISSGGNQYISA-GANATETIVNSGGFQRVNSGAVATGTVLSGGTQNVSSGGSAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTSGATISTIVNSGGIQRVSSGG----VASATNLSGGAQNIYNLGHASNTVIFSG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISGTVSSGGTVSSGETQIVYSGRGNSNATVNSGG-TQIV--NNGGKTTATTVNSSGSQNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MNKAYSIIWSHSRQAWIVASELARGH------GFVLAKNTLLVLAVVSTIGNAFAVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQ--AIATAGLVQA
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adhesin AIDA-I #status predicted
                                                                                                                                                            GB:AE008917;
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25.4%;
                         8.9%;
23.1%;
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                                                                                                                                        16M
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       Score 183.5;
Pred. No. 0.00
38; Mismatches
                                                                                                                                                            PIDN: AAL53053.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 185; DB 2; Pred. No. 0.01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
J.0027;
82;
                                            DB 2;
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                                                                                                                                                          PID: g17983913; GSPDB: GN00190
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                                                                                                                                                                                                                                                                                                          O'Callaghan,
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R.Stover, C.K.; phan, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Xuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lary, S.; Olson, M.V.  Nature 406, 959-964, 2000  A.Tille: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho A; Reference number: A82950; MUID:20437337; PMID:10984043  A; Reference number: A82950; MUID:20437337; PMID:10984043  A; Residues: 1-1018 csrvo- A; Cross references: GB:AE004824; GB:AE004091; NID:99950277; PIDN:AAG07469.1; GSPDB:GN001 A; Experimental source: Strain PAO1 C; Genetics: A; Spathus: PAO1 C; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Conservative 72; Mismatches 209; Indels 163; Gaps 22; Query Match Best Local Similarity 20.3%; Pred. No. 0.026; Matches 113; Conservative 72; Mismatches 209; Indels 163; Gaps 22; AGene: PAO482  Qy 1 MKKYRIIWSALNAWYVSELTRUMFKRASATVKTAVLATLEAT	Oy 179 DDQGNIT-VMYDVNVGDALNVNOLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVN 237
A; Accession: Ac4905 A; Status: Inclaic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-1325 CBLATY A; Residues: 1-1325 CBLATY A; Cross-references: GB; AE000248; GB:U00096; NID:g1787783; PIDN:AAC74583.1; PID:g17877 A; Experimental source: strain K-12, substrain Mc1655 R; Cartwright, P; Timms, M; Lithgow, T; HoJ, P: Hoogenraad, N. BLOChim, Blophys, Acta 1153, 345-347, 1993 A; Title: An Escherichia coli gene showing a potential ancestral relationship to the g A; Reference number: 152440; MUID:g4100243; PHID:8274505 A; Accession: 152440; MUID:g4100243; PHID:8274505 A; Residues: 689-883; K', 885-1316, 'S', 1318-1325 CRESS A; Molecule type: DA; A; Residues: 689-803; K', 885-1316, 'S', 1318-1325 CRESS A; Cross-references: EMBL:X73255; NID:g312392; PIDN:CAA51730.1; PID:g312393 A; Mote: the difference in length is due to a frameshift error at pos 653 C; Cenetics: A; Cenet: USA A; Rota: Liberty Cartery C	Db 298 LDGGPDGKVMVGGALSANALNGPGHGGTVEVRCQAVEVALCTQVNTLASNGLNGTWKIAA 357  Qy 262QFSSVSLGAGADAPTLS

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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 SEQUENCE OF 595-1325 FROM N.A. MEDLINE-94100243; PubMed-8274505; Cartwright P.J., Timms M.W., Lithgow T., "An Escherichia coli gene showing a poter to the genes for the mitochondrial import
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                                                                                                                                                                                                                                           PubMed=9097039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               teria; Gammaproteobacteria;
Escherichia.
ow T., Hoej P.B., Hoogenraad N.J.;
a potential ancestral relationship
import site proteins ISP42 and
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EcoGene; EG11780; yc
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; D90793; BAA15190.1; AL;
; D90794; BAA15197.1; AL;
; X73295; CAA51730.1; AL;
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PS00013; PROKAR_LIPOPROTEIN;
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FVSQNITFLGDKASGIGTLNLMDATSSFDTYGINVGNFGSGIVNVSNGATLNSTGYGFIG
                                          GVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLP--GKSMMAIGGGTYRGEAGYAI--
                                                                                                              SMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKD-NKPVRITNVAPGVKEGDVTNVAQLK
: | | | | | | :::: |
                                                                                                                                                                                                           SKAVAGSSGKVISGNVSPSKGKMDET------
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSVLTTELFEIGSYGTGSLNITDKGYVTSSIVAILGYQAGSNGQVVVEKGGEWLIKNNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLVTAKEVID ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GASLEVDNDQITNIDTDVAYDAYLVGWYGTGVLNILAGGNASLTTITTSVIGANEDSEGT
                                                                                      GLVVSNGGSSLGYG---
                                                                                                                                                                               GELNVSSEGKVDSGIITAG---MKETGTGNITVKDKNSVITNLGTNLGYDGHGEMNISNQ
                                                                                                                                                                                                                                                                                                                                                          SIEFQIGNQGTGEA----TIREGGLYTAENTIIGGNATGIGTLNVQDQDSVITVRRLYNG
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                                                                                                                                                                                                                                                                                                                                                                                                         -----NGQTGQADKFETVTSGTNVTF-----ASGKGTTATVSKDDQGNITVMYD-
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N-ACYL DIGLYCERIDE (POTENTIAL)
N-> K (IN REF. 3).
M-> S (IN REF. 3).
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                       Henderson I.R., Mee
"Antigen 43, a phas
determines colony m
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MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.
Riley M., Collado-Vides J., Glasner J.D.,
Gregor J., Davis N.W., Kirkpatrick H.A.,
                                                                                                                                                                                                                                                                                                                 MEDIINE=97251358; PubMed=9097040; Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampel G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AG43_ECOLI STANDARD; PRT; 1039 AA P39180; P75614; P76360; P97241; Q46771; 01-FEB-1995 (Rel. 31, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Antigen 43 precursor (AG43) (Fluffing prote FLU OR B2000.
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                                                                                                      STRAINE / EMG2;
STRAINE / EMG2;
MEDLINE 97443975; PubMed 9298646;
MEDLINE Robison K., Church G.M.;
                                                                                                                                                                                                                                            STRAIN=ML 308-225;
Henderson I.R., Owen
Submitted (JAN-1997)
                                                                                                                                                                                                                                                                                        Yamamoto Y., Horiuchi T.;
"A 460-kb DNA sequence of the Escherichia
corresponding to the 40.1-50.0 min region
DNA Res. 3:379-392(1996).
          FEMS
                                                                GENE
                                                                                "Comparing the predicted and observed r
in the genome of Escherichia coli K-12.
Electrophoresis 18:1259-1313(1997).
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Bacteria; Proteobacteria; Gammaproteobacteria;
                  determines
K-12.";
                                                      MEDLINE-97257509;
                                                                                                                                                                    43, a unique protein 
Escherichia coli.";
                                                                                                                                                                                      "Purification and
                                                                                                                                                                                                         MEDLINE-89291704;
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                                                                                                                                                           Bacteriol.
Microbiol. Lett. 1 FUNCTION: CONTROLS
                                                                                                                                                                                                                                                                                                                                                                                                                  complete genome sequence ce 277:1453-1474(1997).
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                                                                                                                                                                                                 Owen
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                      , Meehan M., Owen P.;
phase-variable bipartite outer membrane protein,
ony morphology and autoaggregation in Escherichia
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D., Rode C.K., May
., Goeden M.A., Ro
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AND
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EMBL; D90838; BAA15825.1; AI
EMBL; D90839; BAA15832.1; AI
EMBL; U24429; AAB47869.1; -...
HSSP; P07505; 1SRD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF03797; Autotransporter; 1.
Pfam; PF03212; Pertactin; 1.
TIGRFAMs; TIGR01414; autotrans_barl;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produ
sen the Swiss Institute of Bioinformatics
                                                                                                                                                                                                          Similarity
PGGSVSDTVISAGGGQSLQGRAVNTTLNGGEQWMHEGAIATGTVI--
                                                                                                                                                           MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQA-----SAN
                                                                                           NVDFVRTYDTVEFLSADTKTTTVNVE-SKDN--
                                                                                                                           LNTCYRLVWNHMTGAFVVASELARARGKRGGVAVALSLAAVTSLPVLAADIVVHPGETVN
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                              ----AKTSVIKEKDGKLVTGK--DKGENGSSTDEGEGLVTAKEVIDAVNKAGWR-----
                                                              {\tt GGTLANHDNQIVFGTTNGMTISTGLEYGPDNEANTGGQWVQDGGTANKTTVTSGGLQRVN}
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T -> K (IN STRAIN ML 308-225).

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ATN -> STI (IN STRAIN ML 308-225).

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ESCHETICHIA COLL N. 2174 (1991).
BIOCHIMIE 73:1361-1374 (1991).
-I- SIMILARITY: TO S. TYPHIMURIUM ORF NEAR CYSG (AC P25928).
-I- SIMILARITY: TO S. TYPHIMURIUM ORF NEAR CYSG (AC P25928).
-I- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE COD THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEM
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-97251357; PubMed-9097039;
MEDLINE-97251357; PubMed-9097039;
Klitakawa M., Kitagawa M.,
Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura
Makade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,
Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
"A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.
NA Res. 3:363-377(1996).
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P33666; P76087; P76088; P76856; P76857; P76859

01-FEB-1994 (Rel. 28, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                   Moszer I., Glaser P., Danchin A.; "Multiple IS insertion sequences near Escherichia coli K-12.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-97426617; Pubmed-9278503;
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Enterobacteriaceae; Escherichia.
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YDBA OR B1401/B1405.
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092393; 09RB66; 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) 16-0CT-2001 (Rel. 40, Last annotation update) Probable outer membrane protein pmp8 precursor protein 8) (Outer membrane protein 11). PMP8 OR OMP11 OR CPN04446 OR CP0307.

(Polymorphic

PMP8\_CHLPN

STANDARD;

Chlamydia pneumoniae Bacteria; Chlamydiae;

(Chlamydophila Chlamydiales;

pneumoniae).
Chlamydiaceae;

Chlamydophila

NCBI\_TaxID=83558;

SEQUENCE

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PIR; D72078; D72078.
PHCI-2DPAGE; Q9Z393;
TIGR; CP0307; -
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TIGRFAMS; TIGRO1376; POMP_repeat; 6.
Outer membrane; Signal; Multigene family;
                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long a modified and this statement is not removed, entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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Eisen J., Fraser C.M.
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Nucleic Acids Res. 28:2311-2314(2000).
-!- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shirai M., Hirakawa H., Kimoto M., Tabu
Shiba T., Ishii K., Hattori M., Kuhara
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                                                                                                                              SIGNAL
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Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
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MEDLINE=20007584;
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                                                                                             CONFLICT
                                                                                                                                                                                                                                         InterPro; IPR006315; InterPro; IPR005546;
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"Comparison of whole genome sequences of Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20330349;
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AE002193;
AP002546;
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                                                                                                                                                                                            PF03797; Autotransporter; PF02415; DUF145; 2.
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IPR005546; Autotransporter.
IPR003368; Chlamydia_PMP.
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930
                  Conservative
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hara S., Nakazawa
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y K., Bass S.,
Dodson R.,
Salzberg S.
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Gilmore R.D. Jr., Joste N., McDonald G.A.; "Cloning, expression and sequence analysis of 120 kD surface-exposed protein of Rickettsia Mol. Microbiol. 3:1579-1586(1989).
                                                    modified and this statement entities requires a license
                                                                                                                                                                                                                                                                          -!- FUNCTION: MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
-!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Alp
Rickettsiaceae; Rickettsieae;
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Gilmore R.D. Jr.,
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28-FEB-2003
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MISCELLANEOUS: ITS C-TERMINUS POTENTIALLY MAY BEAR THE E
CONFERRING ANTIGENICITY TO THE PROTEIN.
SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                              European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content
                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a deen the Swiss Institute of Bioinformatics and the EMBL
X16353; CAA34402.1;
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                                     equires a license agreement (S email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WEDLINE=90136087; PubMed=2515418;
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coning, expression and sequence analysis of the gene encodir

coning, expression and sequence analysis of the gene encodir

by Surface-exposed protein of Rickettsia rickettsia.";

Microbiol. 3:1579-1586(1989).

Microbiol. 3:1579-1586(1989).

FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR

STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL

VIRULENCE FACTOR AND/OR IMMUNOSEN DURING INFECTION.

SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED

LAND MICROBIOLOGIC CONTRACTOR CONTRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               European Bioinformatics Institute.
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SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
467
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                                                                                                                 407
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                                                          83
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ii is encoded by an unusually long open reading f
for protein processing from a large precursor.";
robiol. 5:2361-2370(1991).
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1654
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There are no restrictions
ng as its content is in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BIGA_SALTY STANDARD; PRT; 19
P25927; P25928; Q9XCQ3;
Q1-MAY-1992 (Rel. 22, Created)
28-FEB-2003 (Rel. 41, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Putative surface-exposed virulence pro
BIGA OR STM3478.
                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                               MEDLINE=91100301; pubMed=1987123; Wu J.Y., Siegel L.M., Kredich N.M.;
                                                                                                                                                                                                                                                                         Nature
[3]
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"Salmonella typhimurium
Submitted (MAR-1999) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-ATCC 14028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella typhimurium.
Bacteria; Proteobacteria;
Enterobacteriaceae; Salmon
                                                                                                                                                                                                                                      STRAIN-LT2;
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MEDLINE-21534948; PubMed-11677609;
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                                                                                                                                               cofactor."
                                                                                                                                                             requirement
                                                                                                                                                                                                                                                                                                                        "Complete genome
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                                                                                                        Bacteriol. 173:325-333(1991).
CAUTION: Ref.3 sequence differs
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                                                                                     UTION: Ref.3 sequence c
positions 414 and 732.
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imurium rhs homolog.";
999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                        sequence of Salmonella enterica serovar Typhimurium
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cysG plasmid
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ou S., Layman [
, Mulvaney E.,
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modified and this statement is not removentities requires a license agreement (S or send an email to license@isb-sib.ch).
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M64606; AAA27043.1;
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                                                                                                                                                                                                                                                    VWNYSEQDNQW----
                  GKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIK-GTASGNSRGHFGASA----SVGY
                                                  PVRITNVAPGVK-EGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLP
                                                                                 T-DGGTGGHITGDNVVIDNAGSTTV----
                                                                                             NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD---ALNVGSKKDNK
                                                                                                                                                                                                            LIIADDNTTVISGDDQAHNSDRGMDISG-----QDRTGVIISG-DRTVNTLTGDSSVTDG
                                                                                                                                                                                                                                L-SADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGEN-----GSSTDE
                                                                                                                                                                                                                                                                       IWNSAL--NAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANNVDFVRTYDTVEF
                                       --TISGGAVGTRIDGDDAHTTNTGDIA--
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1 (INCOMPLETE).
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Pred. No. 1
GDLLVTDGAMGIITYGT--GNEAKNTGNATVRDADSVGF
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                                       VDGAGSAAVIINGDNGSLTQA---
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01-JUN-1994 (Rel. 2
01-OCT-1994 (Rel. 3
S-layer protein (SU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blaser M.J., Gotschlich E.C.;
J. Biol. Chem. 265:19372-19372(1990).

-i- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. THIS PROTEIN IS
CRITICAL FOR VIRULENCE.
-i- SUBCELLUILAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
S-LAYER WITH HEXAGONAL SYMMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; J05577; AAA23032.1;
Cell wall; S-layer.
SEQUENCE 933 AA; 96757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstatise the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/announcement an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteraceae; Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blaser M.J., Gotschlich
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MEDLINE=90354448; PubMed=2387868;
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                                                      V-NAKLTDVTSIIIDGMQITLGHAGTAGTDYSKVSMIDASALKAGLTFDASAI-TLG---
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                          AYLPGKSMMAIGGGTYRGEAGYAIGYSSIS-DGGNWIIKGTASGN
                                                                                  APGVKEGDVTNV----AQL---
                                                                                                                                                                                                                                             GQTGQADKFETVTSGTNVTFASGKGTTATVSK--DDQGNITVMYDVNVGDALNVNQLQNS
                                                                                                                                                                                                                                                                                   ----SGKTLVIKGAEVETLVNID
                                                                                                                                                                                                                                                                                                                                      KRAAAKVKLNTTAATDQTVTLKANA-----TDNSLEFDSATAKTTSVTASG-----
                                                                                                            NDVTALMIVVKIVLDAÄAKDTNIALGTAAADKALVIDTGIETLNITSLVKATSPETTANT
                                                                                                                                                                    ENVAISDAVATADLSSSAFKNSVIITTKEAADTTLTINKDQVINFTAADAGSVKLITVKL
                                                                                                                                                                                            GWNLDSKAVAG --- SSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKN-
                                                                                                                                                                                                                          GKTGQGGKF-SVKTGTGDDKIEFVGTTLTEGSVIDAPGNDTIAMKSAALTSANFTMIKNI
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    Created)
    Last sequence update)
    Last annotation update)
    SAP)

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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 143;
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                                                                                -KGVAQNLNNRIDNVDGNA-RAGI---AQAIATAGLVQ
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RESULT 10
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InterPro; IPR001029; Flagellin_C.
InterPro; IPR001492; Flagellin_C.
Pfam; PF00700; Flagellin_C; 1.
Pfam; PF00669; Flagellin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboratio between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entitles requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J.
Yang J., Yang E., Zhang X., Zhang J., Yang G., Wu H., C
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding R
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen
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Bacteria; Proteobacteria; Gammachanteriaceae; Shigella.
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01-NOV-1995
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"Genome sequence of Shigella flexneri 2a: insights into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tominaga A., Mahmoud M.A.-H., Mukaihara "Molecular characterization of intact, in the genus Shigella.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Flagella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS;
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    NLDSKAVAGSSGK - -
                                                                                                                                                                                       VIKEKDGKLYTGKDKGENGSSTDEGEGL---YTAKEVIDAVNKAGWRMKTTTANGQTG--
                                                                                                                                                                                                                                        TVQASTGTNSDSDLDSIQDEIKSRLDEIDRVSGQTQFNGVNVLAKDGSMK - - IQVGANDG
                                                                                          QADKFETVTSGTNV--TFASGKGTTATVS--KDDQGNITVMYDVNVGDALNVNQLQNSGW
                                                                                                                                           QTITIDLKKIDSDTLGLNGFNVNGGGAVANTAASKADLVAANATVVGNKYTVSAGYDAAK
                                              ASDLLAGVSDGDTVQATINNGFGTAASATNYKYDSASKSYSFDTTTASAADVQKYLTPG-
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SEQUENCE FROM N.A., AND SEQUENCE FROM N.A., AND SEQUENCE FROM N.A., AND SEQUENCE FROM N.A., SMIT J.
T.A., SMIT J.
T.A., AND SEQUENCE FROM N.A., AND SEQUENCE FROM N.
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P35828; Q46015; Q9RF12;
01-JUN-1994 (Rel. 29, Created)
16-OCT-2001 (Rel. 40, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
S-layer protein (Paracrystalline surfa
RSAA OR CC1007.
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"The Caulobacter crescentus paracrystalline S-layer protein secreted by an ABC transporter (type I) secretion apparatus. J. Bacteriol. 180:3062-3069(1998).
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MEDLINE=21173698; PubMed=11259647;
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Awram P., Smit J.K.;
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MISCELLANEOUS: THE CALCIUM BINDING OF THIS PR
SURFACE ATTACHMENT BY IONIC BRIDGING BETWEEN
SPECIFIC MEMBRANE-ASSOCIATED OLIGOSACCHARIDE.
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SUBCELLULAR LOCATION: CELL WALL, THIS BACTERIUM IS COVERED BY A LAYER WITH HEXAGONAL SYMMETRY. SECRETED BY AN ABC TRANSPORTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collable en the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
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"Bridence for proteolytic cleavage of the 120-kilodalton outer
membrane protein of rickettsiae: identification of an avirulent
mutant deficient in processing.";

Infect. Immun. 60:159-165(1992).

-1- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.

-1- FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.

-1- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.

-1- SUBCELJULAR LOCATION: CELL MAIL. THIS BACTERIUM IS COVERED BY A
S-LAYER WITH HEXAGONAL SYMMETRY.

-1- SUNCLULURA LOCATION TO THE RICKETISIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Wilmington;

MEDLINE=940440787; PubMed=8224886;

Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;

"Cloning and sequence analysis of the gene encoding surface layer protein of Rickettsia typhi.";

Gene 133:129-133(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Surface protein antigen) (rOmp B) [Contains: 120 kl antigen) (120 kDa outer m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content
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                                                SEQUENCE
                                                                                                                                                                                                                                              Antigen;
                                                                                                                                                                                                                                                                        TIGRFAMS;
                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an
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15-JUL-1998 (Rel.
16-OCT-2001 (Rel.
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Match
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                                                                                                                                                                                                                                                                                               Pro; IPR005546; Autotransporter. PF03797; Autotransporter; 1.
                                                                                                                                                                                                                                            S-layer;
                                                                                                                                                                                                                                                                                                                                                                                                                                            requires a license agreement (See http://www.isb-sib.ch/announce/
nn email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and this statement is not removed.
                                                                                                                                                                                                                                                                   3797; Autotransporter; 1. TIGR01414; autotrans_barl; 1.
                                                                                                                                                                                                                                                                                                                                        IPR006315; Autotransport
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                                                                       1415
657
842
1071
1306
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21. 36, Last sequence update)
el. 40, Last annotation update)
21. protein B precursor (168 kDa surface-layer protein)
22 in antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
23 in antigen) (Cell surface antigen 5) (Surface protein
24 cains: 120 kDa surface-exposed protein (Surface protein)
25 cains: 120 kDa surface-exposed protein (Surface protein)
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                                         Transmembrane; Cell wall.
1353
120 kDa SURFACE-EXPOSED PROTEIN.
1645
32 kDa BETA PEPTIDE.
1429
MEMBRANE ANCHOR (POTENTIAL).
657
H -> N (IN REF. 2).
842
V -> I (IN REF. 2).
1306
G -> S (IN REF. 2).
1306
G -> S (IN REF. 2).
1306
G -> S (IN REF. 2).
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RICCN STANDARD;
OMPB_RICCN STANDARD;
O9KKA3; O9KK98; O9XC45;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
Outer membrane protein Surface antigen 5) (Sca5) (rompb)
Outer membrane protein Surface antigen 5) (Sca5) (rompb)
Outer membrane protein Surface protein (Surface protein)
Outer membrane protein ompb); 32 kDa beta peptide]
STRAIN=Malish
Stenos J., Wa
                           SEQUENCE
                                                                Roux V., Raoult D.;
"Phylogenetic analysis of membegene coding the outer-membrane
                                                                                                        STRAIN=Indian tick typhus, and Mal MEDLINE=20393643; PubMed=10939649;
                                                                                                                                 SEQUENCE OF
                                                                                                                                                            Science
                                                                                                                                                                                                Ogata H., Audic S.,
Samson D., Roux V.,
                                                                                                                                                                                                                                           SEQUENCE FROM STRAIN=Malish
                                                                                                                                                                                                                                                                                  Rickettsiaceae; Rickettsieae; NCBI_TaxID=781;
                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                      Raoult D.
                                                                                                                                                                                                                             MEDLINE=21442074;
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                           OF 353-1655
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c., Renesto-Audiffren
c., Cossart P., Weisse
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                                                   members of the genus Ribrane protein rOmpB (ompbiol. 50:1449-1455(2000)
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                                                                                                                                                                           Rickettsia
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EMBL; AF123721; AAF34124.1;
EMBL; AF123726; AAF34129.1;
EMBL; AF149110; AAD39533.1;
PIR; E97835; E97835.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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-!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL STRUCTURAL PROTEIN WHICH STRUCTURAL PROTEIN FUNDER TOWN THE TO
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SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE
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RITHVAPGVKEGDVTHVAQLKGVAQNLHHRIDHVDG-NARAGIAQAIATAGLVQ-----
                                               QFAHNTYLITRTTNAAGQGKIIFNPVVNNNTTLATGTNLGSATNPLAEINFGSKGAANVD
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                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                    This
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01-APR-1990 (Rel.
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Enterobacteriaceae; Serrat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: CELL-BOUND HEMOLYSIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYT
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SVSGNKVSFLAADDKTASNTEQTKIGGGFYYTGGIDKLGSGVEAGYENNKTQAQSSKAIT
                     VTSGTNVTFASGKGTTA--
                                                                                                                                                             ELTRNH - - - - TKRASATVKTAVLATLLFATVQASANNVDFVRTYDTVEFLSADTKTTTV
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                                            KEAGDKQYRAGLRIEHTRDSEKTTRTENSASSLSGGSVKLKAEKDVTFSGSKLVADKGDA
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                                                                                                                                                                                                                                                                   Toxin;
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                                                                                                                                                                                                                                   1608 AA;
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                                                                                                                                                                                                                                                                                                                                                             Bioinformatics Institute.
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BACTERIAL HEMOLYSINS ARE
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J. Bacteriol. 176:3295-3302(1994).

-I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1994 (Rel. 30, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Amylopullulanase precursor (Alpha-amylase/pullulanase) (Pullulanase type II) [Includes: Alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase); Pullulanase (EC 3.2.1.41) (1,4-alpha-D-glucanohydrolase); Pullulanase (EC 3.2.1.41) (1,4-alpha-D-glucanohydrolase); Pullulanase (EC 3.2.1.41) (1,4-alpha-D-glucanohydrolase); Pullulanase (EC 3.2.1.41) (1,4-alpha-D-glucanohydrolase); Pullulanase (EC 3.2.1.41) (1,4-alpha-D-gluca
 InterPro;
InterPro;
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                                     EMBL; M57692;
HSSP; Q08751;
                                                                                            or send an
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STRAIN-DSM 3896 /
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01-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matuschek M., Burchhardt G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94252998; PubMed=8195085;
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                                                                                                                                                                                                                                SIMILARITY: Contains 2 fibronectin type III domains. SIMILARITY: Contains 3 S-layer homology (SLH) domains.
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                                                                                              email to license@isb-sib.ch).
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 Alp_amyl_cat_sub Alpha_amyl_C.
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SMART; SM00632; Aamy_C; 1.
SMART; SM00060; FN3; 2.
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PF02922; isoamylase_N;
PF00395; SLH; 3.
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                                                     VTLNISKANDPRKVA----VYYYNPTTNQWEYVGGKVDASSGTITFNATHFSQYAAFEYD
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IPR003961; FN_III.
IPR004185; Glyco_hydro_13Ig
IPR004193; Glyco_hydro_13N.
IPR001119; SLH.
                        IGYSSISDGGNW---IIKGTAS
                                                                             ----ARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAG----
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FIBRONECTIN TYF
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FIBRONECTIN TYPE-III
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1: sp_archea:*
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8: sp_organel:
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
11: sp_rodent:
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## ALIGNMENTS

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MEDLINE=20175755; pubMed=10710307; Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Eisen W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,	"Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing."; Science 287:1816-1820(2000). [2] SEQUENCE FROM N.A. STRAIN=MC58 / Serogroup B;	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.:	meningitidis, and meningitidis (serogroup B). Proteobacteria; Neisseriales; eae; Neisseria. Betaproteobacteria; Neisseriales; eae; Neisseria. Proteobacteria (Neisseria). Proteobacteria; Neisseriales; Neisseriales	JIT 1  218  Q9JR18 PRELIMINARY; PRT; 591 AA.  Q9JR18;  O1-CCT-2000 (TrembLrel. 15, Created)  O1-CCT-2000 (TrembLrel. 15, Last sequence update)  O1-CCT-2002 (TrembLrel. 22, Last annotation update)  Outer membrane protein GNA992 (Adhesin) (NhhA outer membrane  protein).  GNA992 OR NMB0992 OR NHHA.

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O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
e genome sequence of Neisseria meningitidis serogroup
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Comanducci M., Jennings G.T., Baldi L., Bartolini E., C
Galeotti C., Luzzi E., Manetti R., Marchetti E., Mora
Ratti G., Santini L., Savino S., Scarselli M., Storni E
Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tet
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M.,
Moxon E.R., Grandi G., Rappuoli R.,
"Identification of Vaccine Candidates Against Serogroup
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Bacteria;
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EMBL; AF226366; AAF42515.1; -.
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Pfam; PF03895; YadA; 1.
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Pfam; PF03895; YadA; 1
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"Identification and characterization of a gene
membrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ of
EMBL; AF157606; AAK68867.1;
Interpro; IPR005594; YadA.
Pfam; PF03895; YadA; 1
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Bacteria; Proteobacteria;
Neisseriaceae; Neisseria.
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"Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";

Science 287:1816-1820(2000).

EMBL; AF226371; AAF42520.1; -.

InterPro; IPR005594; Yada.
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Science 287:1816-1820(2000).
EMBL; AF226361; AAF42510.1; -.
Interpro; IPR005594; YadA.
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"Identification of Vaccine Candidates Against Serogroup B
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MEDLINE=20175756; PubMed=10710308;
Masignani V.
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ceae; Neisseria.
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. 15, Last sequence up
. 22, Last annotation
GNA992.
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Pred. No. 1.2e
2; Mismatches
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"Identification of Vaccine Candidates Against Se;
Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
EMBL; AL162755; CAB84461.1; -.
EMBL; AF26357; AAF42508.1; -.
EMBL; AF226357; AAF42514.1; -.
EMBL; AF226386; AAF42514.1; -.
EMBL; AF226386; AAF4253.1; -.
EMBL; AF226386; AAF4253.1; -.
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Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd
Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis Z2491.";
Nature C.
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01-0CT-2000
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STRAIN-205900, BZ133, F6124, AND Z2491;

MEDLINE-20175756; PubMed-10710308;

Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.

Galeotti C.L., Luzzi E., Manchetti E., Mora M., Nuti

Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Z2491 / Serogroup A / Serotype MEDLINE=20222556; PubMed=10761919;
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Putative surface :
NMA1200 OR GNA992
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000 (TrEMBLrel 15, Last sequence update)
002 (TrEMBLrel 22, Last annotation update)
surface fibril protein (Outer membrane pro
GIGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNIKGVKTGSTTGQSENVDF
                                                                                                                      NASSFTYSLKKDLTGLINVETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN
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Pred. No. 3.7e
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                                                                                                                                                                                                          MEDLINE=20175756; PubMed=10710308;

A Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

A Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.

A Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.

A Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti

A Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

A Brocker M., Hundt E., Knapp Bs., Blair E., Mason T., Tettelin H.,

A Hood D.W., Jeffies A.C., Saunders N.J., Granoff D.M., Venter C.,

A Moxon E.R., Grandi G., Rappuoli R.,

"Identification of Vaccine Candidates Against Serogroup B

Meningococcus by Whole-Genome Sequencing.";

Science 287:1816-1820(2000).

EMBL, AF226378; AAF42527.1;

R Pfam, PF03895; YadA, 1.
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01-OCT-2000
01-OCT-2000
01-OCT-2002
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Bacteria; Proteobacteria;
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                                                                                                                                                                                                SEQUENCE
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(TIEMBLrel. 15, Last sequence update)
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ane protein GNA992.
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67.1%;
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TNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGI

51

Duely match  91.0%; Score 1890.3; Length 398; Best Local Similarity 66.4%; Pred. No. 5.1e-83; Matches 397; Conservative 2; Mismatches 8; Indels 191; Gaps 2;  Qy  1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQAS 50	DIRECE FROM N.A.  MAIN-SWZ107;  MAIN-SWZ107;  MAIN-SWZ107;  MASIGNANI V., Giuliani M.M., Arico' Bardolici M., Scarlato V., Masignani V., Giuliani M.M., Arico' Bardolici M., Scarlato V., Masignani V., Giuliani M.M., Arico' Bardolici M., Scarlato V., Mancetti R., Bartoliti E., Capecc leotti C.L., Luzzi E., Mancetti R., Marchetti E., Mora M., Liti G., Santini L., Savino S., Scarselli M., Storni E., Zu beker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin John, Jeffries A.C., Saunders N.J., Granoff D.M., Vente Con E.R., Grandi G.), Rappuoli R.;  Mentification of Vaccine Candidates Against Serogroup B lingococcus by Whole-Genome Sequencing.";  Mentification of Vaccine Candidates Against Serogroup B lence 287:1816-1820(2000).  Mi, AF226385; AAF42534.1;  Merroro IPR005594; YadA.  Mi, PP03895; VadA; 62431 MW; 0881CC094F33B4D4 CRC64;  MATCH CANACA CANACA CANACA CANACA CRC64;	JPF		Qy 179 DDQGNITVMYDVNVGDALNVNOLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNI 238	Qy  181 GSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVR 58  181 GSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVR 240  Qy  59 TYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTD 118  111111111111111111111111111111111
DR InterPro; IPRO05594; Yada; 1.  DR Pfam; PF03895; Yada; 1.  SQ SEQUENCE 595 AA; 62120 MW; 8212C96380142BFC CRC64;  Query Match 91.6%; Score 1890; DB 2; Length 595;  Hest Local Similarity 66.6%; Pred. No. 5.4e-83;  Matches 396; Conservative 4; Mismatches 7: Indels 188; Gaps 2;  Matches 396; MAKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASA		J PH T	Qy 231 KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDG-DALNVGSK 289	Qy 111 GENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGK 170	Qy       51 50         Db       121 NTDENTNASSETYSLKKDLTDLTSVETEKLSFGANGKKVNITSDTKGLNFAKETAGTNGD 180         Qy       51 50         Db       181 TTVHLNGIGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNIKGVKTGSTTGQ 240         Qy       51 ANNVDEVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDK 110         Pb       241 SENVDEVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGK 300

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A Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,
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A Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
A Moxon E.R., Grandi G., Rappuoli R.,
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Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
R EMBL; AR226379; AAR42528.1;
R Interpro; IPR005594; YadA;
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InterPro; 1:..
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Q93QY4;
                                   Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennir "Identification and characterization of a gene encoding membrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF157605; AAK68866.1; -.
InterPro; IPR005594; YadA.
Pfam; PF03895; YadA; 1.
SEQUENCE 594 AA; 62297 MW; 9DDD48B04B3A8EA2 CRC64;
                                                                                                                                     Bacteria; Proteobacteria;
Neisseriaceae; Neisseria.
NCBI_TaxID=487;
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Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecch
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., N
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo
Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter
Moxon E.R., Grandi G., Rappuoli R.;
"Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
                                                                                                                                                                                                         Science [2]
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Outer membrane protein GNA992 (NhhA outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM STRAIN=NGH38;
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Neisseriaceae; Neisseria.
NCBI_TaxID=487;
                                  Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennir "Identification and characterization of a gene encoding membrane protein of Neisserla meningitidis."; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
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STRAIN-NG3/88, and BZ232;
MEDLINE-20175756; PubMed=10710308;
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Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico Comanducci M., Jennings G.T., Baldi L., Bartolini E., Caf Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora J Galeotti C.L., Luzzi E., Wanto S., Scarselli M., Storni E., Knapp B., Blair E., Mason T., Tett
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Neisseriaceae; NCBI\_TaxID=487;

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"Identification of Vaccine Candidates Against Serogroup Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
EMBL; AF226369; AAF42528.1; -.
EMBL; AF226369; AAF42518.1; -.
InterPro; IPR005594; YadA.
Pfam; PF03895; YadA; 1.
                                                                                                       Neisseria meningitidis.
Bacteria; Proteobacteria;
Neisseriaceae; Neisseria.
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Neisseria meningitidis, useful in producing vaccines for t
preventing broad spectrum of Neisseria meningitidis -
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 AGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDA
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                                                                              meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167) encoding the proteins. Compositions comprising the protein, nucleic acid or antibody specific to the protein are useful as pharmaceuticals, e.g. a vaccine composition or a diagnostic composition. The composition is also useful for treating or preventing an infection due to Neisserial bacteria, especially Neisseria meningitidis.
                                                                                                                                                                                   New protein and its nucleotide sequence, useful in vaccines or diagnostic compositions for treating and/or preventing Neisseria meningitidis infections
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                                                                                                                                                               Claim 1; Page 62; 123pp;
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98GB-0000760.
98GB-0019015.
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                                                                                                                                                               English.
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                    Score 2108; DB 20;
Pred. No. 6.2e-131;
0; Mismatches 0;
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Neisseria meningitidis meningitidis infections
                                                                                                                                                                                                                           Surface protein;
                                                                                                                                                                                                                                              A surface protein of Neisseria meningitidis.
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                                                                                INNOVATION QUEENSLAND.
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                                                             Moxon
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                                                                                                               97GB-0026398
                                                                                                                                  98WO-AU01031
                                                                                                                                                                                                                           surface
                                                                                                                                                                                                                                                                                                          Protein;
                                                             ER,
           surface
                                                                                         LTD
                                                             Peak
                                                                                                                                                                                                                           glycoprotein;
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                                                             IRA;
          proteins useful
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                                                                                                                                                                                                                            infection;
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591 433

for

vaccine;

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RESULT 5
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Best Local Sim
Matches 433;
Neisseria meningitidis
                          Surface antigen NhhA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kba. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans.
                                                                            24-OCT-2001
                                                                                                                                AAU06171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especial in the form of vaccines. The proteins and antibodies can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
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                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                           NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASAN-------
                                                                                                                                                                                           MAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 127-128; 132pp; English
                                                                                                                                                                                                                                                         ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM
                                                                                                                                                                                                                                                                                                                                               SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL
                                                                                                                                                                                                                                            ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM
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                                                                           (first entry)
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                                                   PMC21
                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.9%;
73.3%;
                          meningococcal
                                                  surface antigen NhhA polypeptide sequence
  strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 2108; D)
Pred. No. 6.2e
0; Mismatches
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                                                                                                                                A
                          disease; meningitis vaccine
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5.2e-131;
nes 0;
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhhA (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen NhhA from N. meningitidis strain PMC21 is 1 of 10 NhhA polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                 Claim 9;
                                                                                                                                                                                                    New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                Peak
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DB; AASO9161.
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                      invention
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Best Local Similarity
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                                                                                                                                                                                                   W09931132-A1
                                                                                                                                                                                                                                                                                             Surface
                                                                                                                                                                                                                                                                                                                               A surface protein of Neisseria
                                                                                                                                                                                                                                                                                                                                                                       08-SEP-1999
                                                                                             12-DEC-1997;
                                                                                                                             14-DEC-1998;
                                                                                                                                                                                                                                      Neisseria meningitidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY23737
 Jennings
                                  (UYQU)
                                                                                                                                                                                                                                                                            Surface protein; immunoreactive po
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| MKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR
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 Moxon
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                                                                                                                                                                                                                                                                                         surface glycoprotein; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
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73.3%;
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 IRA;
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                                                                                                                                                                                                                                                                                             vaccine;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-418754/35.
N-PSDB; AAX85788.
                                                                        AAY57045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis surface meningitidis infections
 21-FEB-2000
                                    AAY57045
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                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                               VNINAGNNIEITRNGKNIDIATSMTPQESSVSLGAGADAPTLSVDGDALNVGSKKDNKPV 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 86-87; 132pp;
                                                                                                                                                                                  MMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                                                                                                                                                          RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKS
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                                                                                                                                                               MMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                                                                                                                                      RITHVAPGVKEGDVTHVAQLKGVAQNLHHRIDHVDGHARAGIAQAIATAGLVQAYLPGKS
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(first entry)
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73.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 2103.5; DB 20
Pred. No. 1.2e-130;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------RAASVKDVLNAGWNIKGVKPGTTASDNVD
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                                                                                              crelates to BASB029 polynucleotide sequences (AAX39864-Z3985) and polypeptide sequences (AAY57044-Y57045) and their immunogenic fragments. C BASB029 polypeptides are useful in a method of diagnosing a Neisseria c meningitidis infection in a mammal. Compositions containing BASB029 cc polynucleotides and polypeptides are useful for generating an immune response in an animal. A therapeutic composition comprising an antibody cdirected against BABB029 is useful in treating humans with Neisseria cc meningitidis disease. The polynucleotide is useful in the diagnosis of the stage of infection, type of infection, susceptibility to an composition which results from increased or decreased expression of the polynucleotide, and for therapeutic or prophylactic purposes, particularly genetic immunisation. Antibodies against BASB029 cc particularly bacterial infections. The protein is useful in the cccombinant protein is useful for treating infections creening and development of antibacterial drugs. Fused recombinant protein is useful for the stimulation of the immune system of an organism
                                      Query Match
Best Local S
Matches 431
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                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                   Haemophilus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infection;
                                                                                                                                                                                                                                                                                                                                                                         is the Nisseria meningitidis BASB029 amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-053103/04.
DB; AAZ39865.
                                        Similarity 72.9
31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASAN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nisseria meningitidis; surface fibril protein;
                                                                                                                                                                                                                                                                                                                                      B strain H44/76. The BASB029 protein is homologous to the us influenzae surface fibril (HSF) protein. The invention basB029 polynucleofide segments.
                                                                                                                      the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         meningitidis
                                                                                           591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treatment; prevent;
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> 92
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389
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269
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123
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98
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                               Score 2101; UB 21,
Pred. No. 1.8e-130;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from N. meningitidis strain
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                                        Indels 158;
                                                                 Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                           for diagnosis,
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RESULT 8
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                                                                                                                                                                                                         Surface antigen NhhA; meningococcal disease; meningitis vaccine; mutant; mutein.
                                                                                                                                                                                                                                    N. meningitidis PMC21 NhhA deletion mutant #4.
      (UYQU ) UNIV QUEENSLAND
                                                                                 WO200155182-A1
                                                                                                                                Protein
                                                                                                                                                                                                                                                        24-OCT-2001
                                                                                                                                                                                                                                                                          AAU06186;
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                         25-JAN-2000; 2000US-0177917
                                           25-JAN-2001; 2001WO-AU00069
                                                                                                                                                            Key
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                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                      MAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 433
                                                                                                                                                                                                                                                                                                                                                                                            ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
                                                                                                                                                                                                                                                                                                                                            MAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
                                                                                                                                                                                                                                                                                                                                                                                 ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM
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                                                                                                                                                                                      meningitidis
                                                                                                                                                                                                                                                        (first
                                                                                                                     50..502
/label=_Mature_NhhA_deletion_mutant_#4
                                                                                                                                        /label= Signal_peptide
                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                       strain
                                                                                                             "Predicted
                                                                                                   claimed in claim
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                                                                                                     mature protein, claim 12"
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PI DR XX DR

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RESULT 9
AAY23741
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                  AAY23741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence represents N. meningitidis strain PMC21 surface antigen NhhA deletion mutant #4.
                                               AAY23741 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NhhA surface antigen polypeptides and polynucleotides seeria meningitidis, useful in producing vaccines for twenting broad spectrum of Neisseria meningitidis -
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                                                                                                                                                                                                           AQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSIS
                                                                                                                                                                                                                                                                     MTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGV
                                                                                                                                                                                                                                                                                                                                   NQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATS
                                                                                                                                                                                                                                                                                                                                                                                                RMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDALNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGW 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIGSTLTDRAASVKDVLNAGWNIKGVK------NVDFVRTYDTVEFLSADTKTTTVNVE 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KIKQFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASAN------
                                                                                                                                                                                                                                                    MTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGV
                                                                                                                                                                                                                                                                                                                   NQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATS
                                                                                                                                                                                                                                                                                                                                                                              RMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDALNV
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                                               Protein;
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                                               ₿
                                                                                                                            502
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in thumans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The N. meningitidis surface glycoproteins can also be use prevent or treat N. meningitidis infection in humans, espin the form of vaccines. The proteins and antibodies can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A surface protein of Neisseria meningitidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                meningitidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis surface proteins useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9931132-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used to identify immunoreactive peptides.
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361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                           Page 104-106; 132pp; English
                                                           VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
             SKDDQGNITWMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
                                                                                                                         VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
                                                                                                                                                                                      GIGSTLTDTLLNTGATTNYTNDNYTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNYDF
                                                                                                                                                                                                                                                   NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN
                                                                                                                                                                                                                                                                                                                 YLDPVLRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         591 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                      -----RAASVKDVLNAGWNIKGVKPGTTASDNVDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.4%;
72.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2096; DB 20;
Pred. No. 3.9e-130;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IRA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    also be used to humans, especially
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Indels 158; Length

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              WPI; 200
N-PSDB;
New NhhA surface antigen polypeptides and polynucleotides
                                                     UQYU)
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                                                                                                                                                                                                                                                                                                                                                                                              N. meningitidis
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                                                                     25-JAN-2000;
                                                                                    25-JAN-2001; 2001WO-AU00069
                                                                                                                    WO200155182-A1
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                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                                                                               Neisseria meningitidis strain EG329
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               2001-488774/53
DB; AAS09165.
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                                                     ) UNIV QUEENSLAND
                                                                                                                                                                                                                                                                                                                                                                              antigen NhhA; meningococcal disease; meningitis vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
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                                      Jennings MP
                                                                      2000US-0177917
                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                             EG329 surface antigen NhhA polypeptide sequence
                                                                                                                                                                         230..
                                                                                                                                                  /note= "Variable region 4" 237..591
                                                                                                                                                                                                                      /note= "Conserved region 189..210
                                                                                                                                                                                                                                             /label= V2
/note= "Variable region
125...188
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/note= "Conserved
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AAU06183 AAU06183

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RESULT 11
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Best Local S
Matches 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                     MAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                           MAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 433
                                                                                                                                        ITNVAPGYKEGDYTNVAQLKGYAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM
                                                                                                                                                                                  NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR
                                                                                                                                                                                                NINAGNNIEITRNGKNIDIATSMTPQFSSYSLGAGADAPTLSVDGDALNVGSKKDNKPVR
                                                                                                                                                                                                                                            SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
                                                                                                                                                                                                                                                          SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
                                                                                                                                                                                                                                                                                                                                                                VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
                                                                                                                                                                                                                                                                                                                                                                                                                          {\tt GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fig 1; 91pp;
                                                                                                                        ITNVAPGVKEGDYTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM
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72.9%;
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Pred. No. 3.9e
1; Mismatches
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8.9e-130;
hes 1;
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Best Local :
                                                                                                                                                                                                                                                                             meningitidis mutant polypeptides of the surface antigen Nhha (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence represents N. meningitidis strain H41 surface
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                         New NhhA surface antigen polypeptides and polynucleotides Neisseria meningitidis, useful in producing vaccines for the preventing broad spectrum of Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Surface
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                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                       antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mutant;
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)B; AAS09173.
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                                                                                                                                                                                                al Similarity
419; Conserv
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                                                                                                                                                                                                                                                                       NhhA
                                                                                                                                             NVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGKGENGSSTDEGEGLVTAKEVIDAVNK
           NVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNK
                                               TNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTV
                                                                                                                                                            MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASA------
                                                                                              ETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDMLLNTGATTNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                    Fig 6; 91pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jennings
                                                                                                                                                                                                                                                                       sequence represents
A deletion mutant.
                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0177917
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/label= Mature_NhhA_deletion_mutant
/note= "Predicted mature protein, sg
claimed in claim 12"
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                                                            NRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTV
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                                                                                                                                                                                                         93.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              strain
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                                                                                                                                                                                            pred. No. 1.6e
3; Mismatches
                                                                                                                                                                                             DB 22;
1.6e-127;
nes 11;
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RESULT 12
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                                                                                                                                                                                                                                                                 Neisseria
Synthetic.
                                                              New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treat preventing broad spectrum of Neisseria meningitidis -
                                                                                           WPI; 2001-488774/53.
N-PSDB; AASO9174.
                                                                                                                  Peak
                                                                                                                                                                                                                                                                                                            N. meningitidis
                                                                                                                                                                                                                                                                                                                                          AAU06184;
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                                                 Claim 12;
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                                                                                                                                                                                          WO200155182-A1.
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                                                                                                                                                                                                                                                                                       mutant;
                                                                                                                                                                                                                                                                                              Surface
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                                                                                                                 IRA,
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                                                                                                                                                                                                                                                                                       mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                            SSISAGGNWIIKGTASGNSRGHFGASASVGYQW 513
                                                                                                                                                                                                                                                                                                                                                                                                    SSISDGGNWIIKGTASGNSRGHFGASASVGYQW 433
                                                                                                                                                                                                                                                                                                                                                                                                                        ATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATSMTPQFSSYSLGAGADAPTLSYDGD-ALNYGSKKDNKPYRITNYAPGYKEGDYTNYAQ
                                                 Fig 7; 91pp; English.
                                                                                                                                                                                                                                                                       meningitidis
                                                                                                                Jennings MP
                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                            PMC21 NhhA deletion mutant #2.
                                                                                                                                                                                                                                                                                              NhhA;
                                                                                                                                                                                                                             /label= Signal_peptide
52..407
                                                                                                                                                                                                                     /label= Mature_NhhA_deletion_mutant_#2
                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                                              meningococcal
                                                                                                                                                                                                              "Predicted mature
                                                                                                                                                                                                                                                                         strain
                                                                                                                                                                                                         claimed in claim
                                                                                                                                                                                                                                                                                                                                                        407
                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                              disease;
                                                                                                                                                                                                       e protein,
                                                                                                                                                                                                                                                                                              meningitis vaccine;
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhhA (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader

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RESULT 13
AAY23740
ID AAY23
XX AAY23
AC AAY23
XX O8-SE
CT 08-SE
CXX Surfa
CXX Surfa
KW immun
XX Surfa
KW immun
XX Neiss
XX Neiss
XX V993
XX 12-JE
XX 12-DE
XX 13-DE
X
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Best Local S
Matches 407
                                       (ISIS-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effective immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence represents N. meningitidis strain PMC21 surface antigen NhhA deletion mutant #2.
                                                                                                                                                                                                                                                                                                                                                                                      A surface protein
                                                                                                                                                                                                                                                                                                                                                                                                                                   08-SEP-1999
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Jennings
                                                                                                                                                    14-DEC-1998;
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                                                                                                                                                                                                                                        W09931132-A1
                                                                                                                                                                                                                                                                              Neisseria meningitidis.
                                                                                                          12-DEC-1997;
                                                                                                                                                                                                                                                                                                                        immunoreactive peptide
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                                          ISIS
                                                                                                                                                                                                                                                                                                                                            protein;
  ΜP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVIKEKDGKLYTGKDKGENGSSTDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GHFGASASVGYQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSR 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKT
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                                          INNOVATION QUEENSLAND.
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  Moxon
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  Peak
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Pred. No. 1.2e-126;
                                                                                                                                                                                                                                                                                                                                                                                    meningitidis.
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                                                                                                                                                                                                                                                                                                                                               vaccine;
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RESULT 14 AAY57044

AAY57044

standard;

Protein;

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DXXX I

AAY57044; 21-FEB-2000

(first

entry)

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Best Local S
Matches 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        surface glycoproteins, nucleic acids, the primers and optional a thermostable polymerase, or antibodies are useful in a kit f the detection or diagnosis of N. meningitidis infection in hum. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especial in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  meningitidis which is approximately 62 kDa. The N. surface glycoproteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        meningitidis infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
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DB; AAX85792.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
          KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                            DFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                              PVRITNVAPGVKEGDVTNVAQLKGVAQNLNNHIDNVDGNARAGIAQAIATAGLVQAYLPG
                                                           PVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPG
                                                                                                                                            TVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE
                                                                                                                                                                                          SSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA
                                                                                                                                                                                                      SSTDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA
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                                                                                                                                                                                                                                                                                         LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV
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70.9%;
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Pred. No. 6e-1
3; Mismatches
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6e-126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 594;
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n a kit for
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can also
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Best Local :
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                                                                                                                                                                                                                                                                                                              polynucleotides and polypeptides are useful for generating an immune response in an animal. A therapeutic composition comprising an antibody directed against BASB029 is useful in treating humans with Neisseria meningitidis disease. The polynucleotide is useful in the diagnosis of the stage of infection, type of infection, susceptibility to an infection which results from increased or decreased expression of the polynucleotide, and for therapeutic or prophylactic purposes, particularly genetic immunisation. Antibodies against BASB029 por polynucleotides and columnisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is the Nisseria meningitidis BASB029 amino acid sequence from serogroup B strain ATCC13090. The BASB029 protein is homologous to Haemophilus influenzae surface fibril (HSF) protein. The invention relates to BASB029 polynucleotide sequences (AAZ39864-Z39865) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASB029; Nisseria meni
infection; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                              relates to BASB029 polynucleotide sequences (AAZ39864-Z39865) and polypeptide sequences (AAY57044-Y57045) and their immunogenic fragment BASB029 polypeptides are useful in a method of diagnosing a Neisseria meningitidis infection in a mammal. Compositions containing BASB029
                                                                                                                                                                                                                                                                 polynucleotides and polypeptides are also useful for treating infect particularly bacterial infections. The protein is useful in the screening and development of antibacterial drugs. Fused recombinant protein is useful for the stimulation of the immune system of an oxi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Fig 2; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptide from neisseria meningitidis useful treatment or prevention of bacterial infections in
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                                    NTNASSFTYSLKKDLTDLTSVGTEKLSFSANSNKVNITSDTKGLNFAKKTAETNGDTTVH
                                                                                                                                   MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTDDDDLYLE
                                                                                   PVQRTAVVLSFRSDKEGTGEKEVTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE
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70.9%;
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                                                                                                                                                                               Score 2032.5; DB Pred. No. 6e-126; 3; Mismatches
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antibacterial drug.
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213..231
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25-JAN-2001; 2001WO-AU00069

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Query Match 92.5
Best Local Similarity 70.5
Matches 421; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis -
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N-PSDB; AAS09164.
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                                                          PVQRTAVVLSFRSDKEGTGEKEVTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE 120
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Search completed: October 6, 2003, 09:22:33 Job time: 40.1842 secs

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Title: Perfect score:

US-09-771-382-26 2197 1 MNKIYRIIWNSALN

Run

October 6,

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Minimum

Searched:

328717 seqs, Gapop 10.0 ,

Scoring table: Sequence:

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Maximum

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/1

2: /cgn2_6/ptodata/1

3: /cgn2_6/ptodata/1

4: /cgn2_6/ptodata/1

5: /cgn2_6/ptodata/1

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Copyright (c) 1993 - 2003
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/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
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Sequence 2, Appli
Sequence 2, Appli
Sequence 11, Appl
Sequence 11, Appl
Sequence 9, Appli
Sequence 15, Appl
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
UMBBER OF SEQ ID NOS: 33
COETMAND: DATO: 1977-12-12
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US-09-377-155-21
Sequence 21, Application
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US-09-377-155-21
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SEQ ID NO 21
LENGTH: 591
TYPE: PRT
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Best Local Similarity
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US-09-268-347-36

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US-09-377-155-33

US-09-69-974-33

US-09-69-974-33

US-09-268-347-47

US-08-685-467-6

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US-08-685-467-26

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US-09-268-347-28
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Pred. No. 3.7e-165;
0; Mismatches 0;
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Result No.

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Query Match

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US-09-669-974-21
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PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR PPLICATION NUMBER: PCT/AU98/01031
PRIOR PPLICATION NUMBER: ECT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR PPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
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PRIOR FILING DATE: 1997-13-12
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Best Local
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APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
CURRENT FILING DATE: 2000-09-26
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nilarity 73.3%;
Conservative
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Pred. No. 3.7e-165;
0; Mismatches 0;
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US-09-377-155-2
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CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
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  VSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDET
                                                                                                             FVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGVKTSVIKEKDGKLVTGKDKGENGS
                                                                                                                          FVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLYTGKDKGENGS
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Pred. No. 8.7e-165;
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; ORGANISM: Neisseria meningitidis US-09-669-974-2
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US-09-669-974-2
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CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
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Best Local
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LENGTH: 592
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SOFTWARE: PatentIn Ver. :
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VNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV
                                                                    VSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDET
                                                                                                                 STDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTAT
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                                                                                                                                                                                                                                               NGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVD
                                                                                                                                                                                                                                                                                                                QNGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHL
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Pred. No. 8.7e-165;
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; TYPE: PRT
; ORGANISM: Neisseria
US-09-377-155-11
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Best Local Similarity
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SEQ ID NO 11
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CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
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                                                   421
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                                                                  NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR 322
                                                                                                                                                                                                TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV 202
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ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM
                                                                                                                SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
                                                                                                                                  SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV 262
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                                                   NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR
                                                                                                                                                                                                                                                                                                                GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
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APPLICANT: SENINGS, MICHAEL PAUL
APPLICANT: MOXON, E. RICHARD
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 11
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US-09-669-974-11
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                                                                                 NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR 322
                                                                                                                                                    SKDDQGNITWMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV 262
                                                                                                                                                                                                                      TDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
                                                                                                                                                                                                                                                                                                                                     GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
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               ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM
                                                                                                                                  SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
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ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM
                                                                  NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR
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72.9%;
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Pred. No. 3.6e-164;
1; Mismatches 1;
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US-09-377-155-9
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SEQ ID NO 9
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Best Local Similarity
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APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: MOVEL SURFACE AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
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CURRENT FILING DATE: 199-08-19
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TYPE: PRT
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                                                                                   PVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPG
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KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
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                                                                  PVRITNVAPGVKEGDVTNVAQLKGVAQNLNNHIDNVDGNARAGIAQAIATAGLVQAYLPG
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Pred. No. 6.1
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5.1e-159;
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; TYPE: PRT
; ORGANIEM: Neisseria meningitidis
US-09-669-974-9
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US-09-669-974-9
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Best Local S
Matches 421
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
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PRIOR ETLING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR PPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
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Similarity 70.9%;
21; Conservative
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TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSKKDNK
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                                                                                                                    TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANK
                                                           PVRITNVAPGVKEGDVTNVAQLKGVAQNLNNHIDNVDGNARAGIAQAIATAGLVQAYLPG
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RESULT 10 US-09-669-974-15 ; Sequence 15, Application ; Patent No. 6333173

GENERAL INFORMATION:

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US-09-377-155-15
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NUMBER OF SEQ ID NOS: 33
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 599
TYPE: PRT
ORGANISM: Neisseria meningitidis
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Best Local S
Matches 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: US/09/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
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                                                                                                                 421
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                                                                                                              GKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDG-DALNVGS 314
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               AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                        KKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQ
                                                                                                                                                                       ASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKD 135
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AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                        KDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQ
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RESULT 11
US-09-377-155-7
; Sequence 7, Application U
; Patent No. 6197312
; GENERAL INFORMATION:
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APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-10-14
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 15
LENGTH: 599
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Best Local S
Matches 422
APPLICANT:
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Similarity 70.5%;
22; Conservative
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PEAK, Ian
JENNINGS,
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Richard
Michael
                                                        US/09377155
Anselm
Paul
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Pred. No. 6.7e-159;
Prematches 9;
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US-09-669-974-7

Sequence 7, Application US/09669974
Patent No. 633173
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128

FERENCE: 065064/0128 APPLICATION NUMBER:

NUMBER: US/09/669,974

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PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 594
TYPE: PRT
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US-09-377-155-7
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Best Local
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TITLE OF INVENTION: MOVEL SURFACE ANTIGE
EILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377, 155
CURRENT FILING DATE: 199-08-19
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TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSKKDNK
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Pred. No., 2.3e-158;
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US-09-377-155-17
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Matches
                                                                                                                                             Sequence 17, Application US/09377155 Patent No. 6197312
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LENGTH: 5
                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                               APPLICANT: PEAK, Ian Richard APPLICANT: JENNINGS, Michael APPLICANT: MOXON, E. Richard TITLE OF INVENTION: NOVEL SIELE REFERENCE: 055064/0128
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PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
                   CURRENT APPLICATION NUMBER: US/O
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SOFTWARE: PatentIn Ver. 2.0
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JENNINGS, Michael Paul
MOXON, E. Richard
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                                                                  SURFACE ANTIGEN
    PCT/AU98/01031
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Pred. No. 2.3e-158;
2; Mismatches 10;
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; TYPE: PRT
; ORGANISM: Neisseria
US-09-377-155-17
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FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
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Patent No. 6333173
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SOFTWARE: PatentIn V
SEQ ID NO 17
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Best Local :
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APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE
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                   APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-13-12
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NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 17
LENGTH: 592
SOFTWARE:
SEQ ID NO 13
                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                         Sequence 13, Application US/09377155 Patent No. 6197312
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C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: G81133
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Elsen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: G81133
A;Status: preliminary
A:Molocyle type. NAA
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A;Experimental source:
C;Genetics:
A;Gene: NMB0992
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· /. +	7	7.1	7.1	7.2	7.2	7.2	7.2	7.3	7.3	7.4	7.4	7.4	7.4	7.4	7.5	7.5
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T#0014	TAOC14	S41539	AB0480	E90696	C48399	A48658	A83080	E97835	в81989	D85724	T17508	AI0452	G85547	D90697	T31105	I40711
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## ALIGNMENTS

A; Molecule type: DNA A; Residues: 1-591 <TET> Query Match
Best Local Similarity
Matches 433; Conserv 121 NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN: 180 VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS 142 SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV TDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETYTSGTNYTFASGKGTTATV 202 YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120 TDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV Conservative GB:AE002450; ce: serogroup 95.98; 73.38; Score 2108; DB 2; Pred. No. 1.1e-110; 0; Mismatches 0; GB:AE002098; NID:g7226229; PIDN:AAF41395.1; PID:g722 B, strain MC58 Length 591; Indels 158; Gaps 52 52

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probable surface fibril protein NMA1200 [imported] - Neiss C; Species: Neisseria meningitidis C; Date: 05-May-2000 #sequence_revision 05-May-2000 #text_c C; Date: 05-May-2000 #sequence_revision 05-May-2000 #text_c C; Accession: A81888 R; Parkhill, J; Achtman, M.; James, K.D.; Bentley, S.D.; C; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall Nature 404, 502-506, 2000 A; Title: Complete DNA sequence of a serogroup A strain of A; Reference number: A81775; MUID:20222556; PMID:10761919 A; Accession: A81888
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A81888
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A; Experimental source: serogroup
C; Genetics:
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417; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591
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                                                           NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSKKDNKPV
                                                                                                                           SKDDGGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
                                                                                                                                                                                             TDEGEGLYTAKEYIDAVNKAGWRMKTTTANGQTGQADKFETYTSGTNYTFASGKGTTATV
                                                                                                                                                                                                                                                           VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
                                                                                                                                                                                                                                                                                                        GIGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNIKGVKTGSTTGQSENVDF
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                                                                                                            SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
                                                                                                                                                                           TDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
                                                                                                                                                                                                                                            VRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGKGENGSS
                                                                                                                                                                                                                                                                                                                                                                      NASSFTYSLKKDLTGLINVETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM
RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKS
                                            NINAGNNIEISRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPV
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Pred.
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No. 3.66
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3.6e-105;
9;
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Mungall, K.; Quail, M.A.;
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R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weldman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 195
Science 269, 496-512, 195
A;Authors; Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: I64138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adhesin homolog HI1732 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Oct-1997
C;Accession: I64138
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A; Residues: 1-298 <TIGR>
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Best Local S
Matches 87
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87; Conser
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                         TTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKD--KGENGSSTDEGE
                                                                                                                                                                                                                                                                                                                                                   MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQA----
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                                                                                                                                                                                                                                          STEDDIEDSAATKODNKNQALKAGDTLTLKAGKNLKAKLDQGGKSVTFALAKDLDVKTAK 120
                                                                                                                                                                                                                                                                                                                          MNKIFKVIWNVVTQTWVVVSELTRAHTKRTSATVATAVLATVLSATVQAINDAGTFVKVQ
                                                                                STSVTFSPSDIEKTRAATIKDVLNAGWNIKGAKVAGGNTENVDLVAGYDNVEFITGDKNT
                                                                                                                                                              VSDTLTIGGNTPAAGGATPKVSITSTADGLKLAKGTNGDTAVHLNGLASTLPDVTTNTGA 180
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                                                                                                                    SANRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKT
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29.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1.9e
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 345;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2
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                                        147
    291
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                                                                                                                        98
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                                                                                  240
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D82671

C;Accession: D82671 R;anonymous, The Xylella fastidiosa Consortium of Nature 406, 151-157, 2000 surface protein XF1529 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000 the Organization for Nucleotide

Seg

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 bel A;Accession: D82671

A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-2059 <SIM>
A;Residues: 1-2059 <SIM>
A;Cross-references: GB:AE003982; GB:AE003849; NID:g9106554; PIDN:AAF84338.1;
A;Experimental source: strain 9a5c
A;Experimental source: strain 9a5c GSPDB:GN

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.! Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; submitted to GenBank, June 2000 F.A.; Acencio, L.E.A.; Carraro, Ferreira, A.J.S. **.** Alvarenga, R., D.M.; Carrer U . 3

Ferreira, V.C.A.; J.A.; Fraga, 4 .s .; Franca, တ . . . Franco, z î.c.;

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surface protein xF1981 [imported] - xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 (c;Accession: A82615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-1190 <SIM>
A; Cross-references: GB:A
                                                                                        A;Title: The genome sequence of the plant pathogen Xylella fastidiosa A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 be
                                                                                                                                                                                                                                                         RESULT
A82615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Contents: annotation C;Genetics:
                                                      A; Status: preliminary
                                                                       A; Accession: A82615
                                                                                                                                               R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Nature 406, 151-157, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
 Cross-references: GB:AE004017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VVVNDLGLSIVGGASLTLSGINAGSHKITNVTAGTEDTDAVNFSQLKSVSEAVDKGWTLT 1595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVVSELTRNHTKRASATVKTAVLATLLFATVQASA-----NRAASVKDVLNAGWNI-
                                                                                                                                                                                                                                                                                                                              ANTRSHVGVGAGVGYQW 2059
                                                                                                                                                                                                                                                                                                                                                                  GNSRGHFGASASVGYQW 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADAKEAMDAVNLRQLDAVAQKSNLQTDDMRHEINNIEDVFKITKGDSASSVKGMGVNAMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGRNAIASADGSVALGDGAKDGGRGAESYTGKYSGVQNNTVGTVSVGDAAKGETRSISNV 1833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVKATRYYSTNDGGTQGGNYDGDGATGSKATAAGVGTQASGEGAAAVGSGAAASGKGSTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KVG--SDVSLGAMGLFIANGPSVTASGFNAGDKVISHVAVGMADTDAVNVSQLKQAVQSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGEN-----GSSTDEGEGLVTAKEVIDAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASGANGSKVVSGGTVDLKNTDGNLAISKSGDSNDVVFNLSKDFKVDEVTAGNTVVNTDGV 1655
                                                                                                                                                                                                                                                                                                                                                                                                    RETSGGVAAAIATANLPQAYVQGRGMTSVGVSSYQGQSAIAVGVSAVSESGHWVFKFSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGTNAAVSGTESVALGK---NTNVSADNAVAI-GNG----SVADRANSVSVGSG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YDVNVG-DALNVNQL----QNSGWNLDS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----KGVKPGTTASDNVD-----FVRTYDTVEFLSADTK-----TTTVNVESK 106
                                                                                                                                                                                                                                                                                                                                                                                                                         -AGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.5%;
24.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·GSER···--QVTNVAAGTADTDAVNVSQLNQGLITAKQYTDGMVGNLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70;
 GB:AE003849; NID:g9107083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 340.5; DB 2
Pred. No. 3.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -ANGQTGQ---ADKFETVTSGTNV----TFASGKGTTA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173;
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A; Experimental source: strain 9a5c R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer as Neto, E.; Docena, C.; El-Oorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000 A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A.Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miraki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A; Authors: da Silva, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A; Authors: da Silva, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A; Silva, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L., A; Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Contents: annotation C; Genetics:
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                                                                                                                                                                                1060
                                                                                                                                                                                                                                                                                                 1012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LNAG-WNIKGVKPGTTASD-------NVDFVRTYDTVEFLSADTKTTTVN 102
                                                           IAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGH 422
                                                                                                                                                                                                                                                                                                                                                    NIDIATSMTPQFSSVSLGAGADAPTLSV----DGDALNVGSK----KDNKPV--
                                                                                                                                                                                                                                                                                                                                                                                                                VNLRQLDRVAQDANRYVDNKIESLSEGQTF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LNVNQL----QNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGK 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDGATGTRSIAVGVGTLASA----EGATAVGSGAAASGKGSTAIGRNAVASADGSVALGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENG-SSTDEGEGLVTAKEVIDAVNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INAGSQKITNVAAGTADTDAVNLSQLNTAMAGSGAKSVHYYSTYD-----GGTQGGNYN
                                                                                                                                                                                                                                                                                                 ----SATP----IAAGVDATAIGVGATASGADSIAMGNKASASADNAVAIGNHSVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GAKDGARGAESYTGKYSGLQNNTVGTVSVGDASKGETRTVS----NVADAKEAT--DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.2%; Score 335; DB 2; 26.9%; Pred. No. 3.7e-11;
                                                                                                                                                                                                                                        RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNAR----AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                -----VKVNSLNN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 110;
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                                                                                                                                                                                1119
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                                                                                                                                                                                                                                                                                                                                                                                                                1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              973
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                                                                                                                                                                                                                                           362
                                                                                                                                                                                                                                                                                                                                                       321
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VGIGAGVGYQW

A86036

probable adhesin Z5029 [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001 C;Accession: A86036 C;Accession: A86036 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Liler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; EDL93

A; Title: Genome sequence of enterohemorrhagic Escherichia iller, L.; Grotbeck, E.J.; Davis, Nature 409, 529-533, 2001 coli 0157:H7

.; May Apoda

PMID:11206551

A; Status: preliminary A; Reference number: A85480; A; Accession: A86036

A; Dedub. F-----A; Molecule type: DNA A; Residues: 1-1588 <STO> A; Cross-references: GB:AE005174; NID:g12518349; PIDN:AAG58749.1; GSPDB:GN00145; UWGP:

PIDN: AAF84783.1;

GSPDB:GN001

NLDNRVTNLDSRVTNLE  ROWSPSKGKMDETV	QY 153 KEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 205 Db 720 AVGTDSLAMGAKTIVNADAGIGIGLNTLVMADAINGIAIGSNARANHA	QY 108 NGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTA 152  Db 660 LLGALSLGTDGESYRQITNVADGSEAQDAVTVRQLQNAIGAVTTTPTK	QY 49 ASANRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVE-FLSADTKTTTVNVESKD 107 Db 600 DAVASGAGCLALGONSSSSIEGSIALGSGSTSNRAITTGIRETSATSD :  :  :  :  :  :  :  :  :  :  :  -  -  -  -  -  -  -  -  -  -  -  -  -	Query Match 15.0%; Score 329.5; DB 2; Length 1588; Db 547 SQYNESISQLAGDTSETYITENGTGVKYIRINDNGLEGQ-Best Local Similarity 26.1%; Pred. No. 1.1e-10; Matches 118; Conservative 63; Mismatches 177; Indels 94; Gaps 17; Qy 135 DKGENGSSTDEG	ference tal s	SHIDA, T.; HALLOII, M.; SHIHAGAWA, H.  terohemorrhagic Escherichia coli 0157:H7 and genc Q1 31; PMID:11258796  Db	A; Molecole A; Reside A; Reside A; Roside A; Reside A; Cross A; Cross A; Cross A; Cross A; Cross A; Cross A; Genet. A; Cross A; Genet. A		Parkh; , T.; S.; Mo	i o t s	Qy 243 SGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSV 292	Qy       206 DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGS 242       Qy       402 SISDGGNWIIKGTASGNSRGHFGASASVGYQW 433         L:     :     :       :       :         :       :       :       :       :       :       :       :       :       :       :       :     :       :     :     :     :     :   :     :     :     :   :     :	QY 153 KEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 205	QY         108 NGKKTEVKIGAKTSVIKEKDGKLYTGKDKGENGSSTDEGEGLYTA 152         QY         293 SLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQ           11	QY 49 ASANRAASVKDVLNAGWNIKGVKPGTTASDNVDEVRTYDTVE-FLSADTKTTTVNVESKD 107	Query Match 15.0%; Score 329.5; DB 2; Length 1588;  Best Local Similarity 26.1%; Pred. No. 1.1e-10;  Matches 118; Conservative 63; Mismatches 177; Indels 94; Gaps 17;  Qy 206 DQGNITVMYDVNVGDALNVNQLQNS     :    :     :     :     :     : : :     : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : : :   : : : : :   : : : : :   : : : : :   : : : :   : : : : :   : : : :   : : : : :   : : : : :   :	
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IDIATSMTPQFSSV 292
:::| : : |
VNVAQLKSSEAGGV 1440
GTYRGEAGYAIGYS 401
||| ||: |:| |
GTYNGESAVALGYS 1556
                                             AQLKGVAQ----- 346
                                                                                                                                           NSGWNLDSKAVAGS 242
| || || ||
|ASAQGKDSVAIGSG 1380
                                                                                                                                                                                         -GQLKVTDAQVSQN 1321
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nge 18-Nov-2002 ca subsp. enterica serova

f.; Skelton, J.; Stevens,
int Salmonella enterica se ard, D.; Wain, J.; Church Dowd, L.; White, N.; Farr

923; GSPDB:GN00176

1107; ls 278; Gaps 25;

ν	7 I	IIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANRAASVKD 59	
₽ G	427 L	427 LLWDEDTGAFSANHGGSTSKITNVAAGALSEDSTDAVNGSQLYETNQKVDQNTSAIADIN 486	
QΥ	60 -	VLNAGWN	
g G	487 T	487 TSITNIGTDALSWDDEEGAFSASHGTSGTNKITNVAAGEIASDSTDAINGSQLYETNMLI 546	
ΣY	89 -		
do	547 S	547 SQYNESISQLAGDTSETYITENGTGVKYIKTNDNGLEGQDAYATGNGATAVGY 599	
Ωy	135 D	135 DKGENGSSTDEG	
do	600 D	600 DAVASGAGCIALGQNSSSSIEGSIALGSGSTSNRAITTGIRETSATSDGVVIGYNTTDRE 659	
QΥ	155 V	A	
do	660 L	660 LLGALSLGTDGESYRQITNVADGSEAQDAVTVRQLQNAIGAVTTTPTKYYHANSTEEDSL 719	
Ωy	193 A	i	
융	720 A	720 AVGTDSLAMGAKTIVNADAGIGIGLNTLVMADAINGIAIGSNARANHANSIAMGNGSQTT 779	

Seq

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-658 <KUR>
A;Cross-references: GB:Al
C;Genetics:
A;Gene: YP00902
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C;Accession: AH0110

R;ParKhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre, Nature 413, 523-527, 2001
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                                               VSLGAGADAP-----TLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQL
                                                                                                                                                                                                                                                                                              AIG--DGAAASADGSVAIGQGSGDNGRGVENYIG----
                          TAFGSGAKATAANSAALGANSVADRANSVSVGSVGNER---QITNVAPATQGTDAVNFDQL
                                                                                                                                                                                                    SG-----LQATDAVNLRQLDG-----
                                                                                                                                                                                                                                                 TGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNL
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                                                                                                                                                       DSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNI-EITRNGKNIDI--ATSMTPQFSS
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Pred. No. 2.2e-10;
7; Mismatches 174;
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Barrell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to GenBank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajina, J.P.; Krieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins chado, M.A.; Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C. F.G.; Numes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L. A; Reference number: A59328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE003981; GB:AE003849; A;Experimental source: strain 9a5c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nature 406, 151-157, 2000
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C;Species: Xylella fastidiosa
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                       SMTPQFSSVSLGAGADAPTLSV----DGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVA
                                                                                                          WNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAG----NNIEITRNG----KNIDIAT
                                                                                                                                                                                                    ADKFETV----TSGTNVTFASGKGTTATVS-KDDQGNITVMYDVNVGDALNVNQLQNSG
                                                                                                                                                                                                                                                   LGAGSMASELNVISVGGGDGVTGPAVRRIVNVGDGIGNNDAVNKSQLDGVTASVN---DV
                                                                                                                                                                                                                                                                                                LVTGKDKGE-NGSSTDEGEGLV--TAKEVI-----DAVNKAGWRMKTTTANGQTGQ
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                                                                  LGFDSHAKGINSTTVGTQSVSLGQGGVSLGYNSFVGEGSFNGLALGSNSLVLLQGVD---
                                                                                                                                                         AASVKTIALTNQVTGSSVASASGKESTAIGSGAQAVADNTVAF---
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A; Molecule type: DNA
A; Residues: 1-1286 cBEN>
A; Cross-references: EMBL:X65022; NID:g42254; PIDN:CAA46156.1;
A; Cross-references: EMBL:X65022; NID:g42254; PIDN:CAA46156.1;
R; Benz, I.; Schmidt, M.A.
Mol. Microbiol. 6, 1539-1546, 1992
Mol. Microbiol. 6, 1539-1546, 1992
A; Title: AIDA-T, the adhesin involved in diffuse adherence of A; Reference number: S22680; MUID:92326638; PMID:1625582
A; Accession: S22680
A; Accession: S22680
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F;1-49/Domain: signal sequence #status predicted <SIG>F;50-1286/Product: adhesin AIDA-I #status predicted <M
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A;Title: Processing of the AIDA-I precursor: removal of AIDA
A;Reference number: $72657; MUID:97055419; PMID:8899706
A;Accession: $72657
A;Molecule type: protein
A;Residues: 847-856 <SUH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, March 1992 A; Reference number: S28634 A; Accession: S28634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: DAEC C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: strain 2787
R; Suhr, M.; Benz, I.; Schmidt, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein A; Residues: 50-56 <BE3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 037 1200 E.: X65022
A; Cross-references: EMBL: X65022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 839-1286 <BE2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: nucleic acid sequence not
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GWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFS
                                                                                                                                                                                                                                 VKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANG
                                                                                                                                                                                                                                                                                                                                                                                                                                               MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLA--TLLFATVQASANRAASVK 58
                                                                                                                QTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDALNVN---
                                                                                                                                                                                                                                                                                                                                               DVLNAGWNIKGV--KPGTTASDNVDFVRTYDTVEFLSADTKTTTVN---VESKDNGKKTE
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                                                           LSGGAQNIYNLGHASNTVIFSG--
                                                                                                                                                                                                                                                                                       -----NISGTVSSGGTVSSGETQIV-----YSGRGNSNATVNSGGTQIVNNGGKT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                         --TATTVNSSG-----SQNVGTSGATI----STIVNSGGIQRVSSGG----VASATN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.6%;
24.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 189; DB 2;
Pred. No. 0.0059;
7; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                           ----GFVLAKNTLLVLAVVSTIGNAFAV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                           --GNQTI-FSGGITDSTNISSGGQQRVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189;
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: H83135
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A; Residues: 1-1018 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A; Accession: H83135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE004824; GB:AE004091; NID:g9950277; PIDN:AAG07469.1; GSPDB:GN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 VKIGAKTSVIK---EKDGKLVTGKDKG---ENGSSTDEGEGLVTAKEVIDAV---NKAGW 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348 YQHIRNGGIASGTIVNQSGYVNIS-SGGY 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 SVSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNN 350
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                                AADLTLNGRLNASGAKAGLELKAEGAIDINDKIVLGGAGSAL--AMDAGEGHRVNGTASV 472
                                                                                      KKD---NKPVRITNVAPGVK---EG--DVTNVAQLKGVAQNLNNRID----NVDGNARA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGGSANGEIHLSG---GNSLSVNQKVDKLIANWDS--FSVAAGERVIFNQPSSSSIALNR 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MNKCYALVWNVSQGCWNVVSEGSRRRGKPAGAKAAIASVLALLGATALAPAYALPSGGTV
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                                                                                                                                                 IAADKIDVRPSAVSDGVTVHADTLSRNLASTNIELVSTKGDLDLDGSVNWASGNRLGLGS 414
                                                                                                                                                                                                                                                               RIVLDGGPDGKVMVGGALSANALNGPGHGGTVEVRGQAVEVALGTQVNTLASNGLNGTWK 354
                                                                                                                                                                                                                                                                                                                        KVISGNVSPSKGKMDETVNINA-----GNNIEITRNGKNIDIATSMTP---
                                                                                                                                                                                                                                                                                                                                                                                                                                         GNITVMYDVNVGDALN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RFTGPSTNGVLNHGGAITAAEGGSIALLGAQVDNRGTVLAQMGGVGLGAGSDLTLNFDGN 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RMKTTTANGQTGQADKFETVTSGTNVTFAS-------GKGTTATVSKDDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 186.5; DB Pred. No. 0.0061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      - VNQLQNSGWNLDSKAVAGSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 143;
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                                                                                                                                                                                                       -VDGDALNVGS 314
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Larbig,
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M.J.;

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C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-
C;Accession: G64964
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland,
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland,
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
G64964
hypothetical protein b2000 - Escherichia coli (strain K-12)
hypothetical scherichia coli
C; Species: Escherichia coli
C; Species: Secherichia coli
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A;Residues: 1-1091 <BLAT>
A;Residues: 1-1091 <BLAT>
A;Cross-references: GB:AE000291; GB:U00096; NID:g1788298;
A;Experimental source: strain K-12, substrain MG1655
A;Experimental source binding; P-loop
C;Keywords: nucleotide binding; P-loop
F;683-690/Region: nucleotide-binding motif A (P-loop)
RESULT 14
A81019
adhesin/invasin,
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112; Conserv
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                                                                                                           VNGGLFTARGGTLAGTTTLNNGAILTLSGKTVNN
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                                                                                                                                                                                                                                                                            LDVLTGHTATNTRVDDGGTLDVRNGGTATTVSMGNGGVLLADSGAAVSGTRSDGK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNL-DSKAVAGSSGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LNAGWNIKGVKPGTTASDNVDFV-----RTYDTVEFLSADTKTTTVNVESKDNG--KKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LNTCYRLVWNHMTGAFVVASELARARGKRGGVAV----ALSLAAVTSLPVLAADI--V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANRAASVKDV
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                                                                                                                                                 IGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGN 418
                                                                                                                                                                                                                                                                                                                     IDIATSMTPQFSSVSLGA-----GADAPTLSV-----DGDALNVGSKKDNKPVRIT
                                                                                                                                                                                                                                                                                                                                                               NQKGRLQVDAGGTATNVTLKQGGALVTSTAATVTGINRLGAFSVVEGKADNV-VLENGGR
  probable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----AKTSVIKEKDGKLVTGK--DKGENGSSTDEGEGLVTAKEVIDAVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GTLANHDNQIVFGTTNGMTISTGLEYGPDNEANTGGQWVQDGGTANKT
  NMB1994 [imported] -
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21.8%; Pred. No. 0.0067;
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Neisseria meningitidis (strain
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C;Species: Neisseria meningitidis
C;C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2
C;Accession: A81019
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; ri, H.; Olin, H.; Vannathevan, J.; Gill, J.; Scarlatto, V.; Masignani, V.; Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Althors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Moxon,
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cell surface protein [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01
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112; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGN-----ARAGI 363
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                                                                                                                                                                                                                                                                                                          SAAYHVG---
                                                                                                                                                                                                                                                                                                                                                                                               SRG-HFGASASVGYQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIK---
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25.7%;
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A; Title: The genome sequence of the facultative intracellular A; Reference number: AD3252; PMID:11756688
A; Accession: AB3486

A; Accession:

A;Status: preliminary

R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; M.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

#text\_change 01-Feb-2002

G.; Mujer, C.;

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S.; O'Callaghan, pathogen Brucella

D.; Ivanov D.; Let Accession: AB3486

A;Molecule type: DNA
A;Residues: 1-365 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL53053.1;

A; Experimental source: strain

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PID:g17983913;

GSPDB:GN00190

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                                                                                                        368 ATAGLYQAYL----PGKSMMAIGGGTYRGEAGYAIG-----YSSISDGGNW 409
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STRAIN=0126:H27 / 2787;
MEDLINE=92326638; PubMed=1625582;
Benz I., Schmidt M.A.;
Benz I., Schmidt M.A.;
"AIDA-I, the adhesin involved in diffuse diarrhoeagenic Escherichia coli strain 27
synthesized via a precursor molecule.";
MOI. Microbiol. 6:1539-1546(1992);
-i- FUNCTION: THIS IS AN ADHESION PROTEIN
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01-JUN-1994
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Enterobacteriaceae; Escher
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## ALIGNMENTS

(Rel. 29, Created)
(Rel. 29, Last sequence up
(Rel. 41, Last annotation

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ceria; Gammaproteobacteria; Enterobacteriales; Escherichia.

diffuse adherence of t strain 2787 (Ol26:H27),

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PROTEIN NECESSARY FOR THE DIFFUSE ENTEROPATHOGENIC ESCHERICHIA COLI

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1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLA--TLLFATVQASANRAASVK 58

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Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K. Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiichi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl.
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew (
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D
Gregor J., Shao Y.;
                                                                                                                                       CORRESPONDING to the 40. DNA Res. 3:379-392(1996)
                                                                                                                                                                                                                                                                                                                      STRAIN=K12;
MEDLINE=97251358;
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Pfam; PF03797; Autotransporter; 1.
Pfam; PF03212; Pertactin; 1.
TIGRPAMS; TIGR01414; autotrans_barl;
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MEDLINE=97443975; PubMed=9298646;
Link A.J., Robison K., Church G.M.;
"Comparing the predicted and observed properties in the genome of Escherichia coli K-12.";
Electrophoresis 18:1259-1313(1997).
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Henderson I.R., Meehan M., Owen P.
Henderson I.R., a phase-variable bipe
"Antigen 43, a phase-variable bipe
determines colony morphology and a
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RESULT 3

YDEK_ECOLI STANDARD; PRT; 1325 AA.

ID YDEK_ECOLI STANDARD; PRT; 1325 AA.

AC P32051; P76140; P77168;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical lipoprotein ydek precursor (ORFT)

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Blatther F.R., Plunkett G. III, Bloch
Riley M., Collado-Vides J., Glasner J.
Science
                          Gregor J.,
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                                                                                                 Enterobacteriaceae;
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CONFLICT
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MEDLINE-97251357; PubMed=9097039;
Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itc
Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
Kasai H., Kashimoto K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Sait
Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,
Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
"A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
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SEQUENCE FF
STRAIN-K12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Membrane; Complete proteome.
SIGNAL 19 1325 HY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D90793; BAA15190.1;
EMBL; D90794; BAA15197.1;
EMBL; X73295; CAA51730.1;
PIR; A64905; A64905.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EcoGene; EG11780; ydek.
PROSITE; PS00013; PROKAR_LIPOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochim. Biophys. Acta 1153:345-347(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: SOMI ISP42 AND MOM38
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SIMILARITY:
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176
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NVEGEDSVLTTELFEIGSYGTGSLNITDKGYVTSSIVAILGYQAGSNGQVVVEKGGEWLI
                                                                                                                                                                                                                                                                        MNKIYRIIWNSALNAWVVVSELTR------NHTKRASATVKTAVLATLLFATVQASAN
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                                      TDEGEGLVTAKEVID---
                                                                         DSEGTYNVLGGTWRLYDSGNNARPLNVGQSGTGTLNIKQKGHVDGGYLRLGSSTGGVGTV
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21.8%;
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M -> S (IN REF. 3).
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ancestral relationship
e proteins ISP42 and
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Bacteria; Proteobacteria;
Rickettsiaceae; Rickettsi
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01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein A precursor (190 kDa anantigen) (rOmpA) (rOmp A).
                                    CHAIN
                                                      Antigen;
                                                                                                                                                    modified and this statement
                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collab
between the Swiss Institute of Bioinformatics and the EMBL outsi
the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                      MEDLINE=90354033; PubMed=2117568; Anderson B.E., McDonald G.A., Jon
                                                                                                                                                                                                                                                                                                                                                                                                                                    OMPA_RICRI
P15921;
                          DOMAIN
                                                                TIGRFAMs;
                                                                               InterPro; IPR006315; Autotransport.
InterPro; IPR005546; Autotransporter.
                                                                                                      PIR; A41477; A41477
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SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY
PF03797; Autotransporter; 1.

PAMS; TIGR01414; autotrans_barl; 3.

PAMS; TIGR01414; autotrans_barl; 3.

PAMS; TIGR01414; autotrans_barl; 3.

POTENTIAL.

1 28 OUTER MEMBRANE PROTEIN A.

1 29 2249 OUTER MEMBRANE TANDEM REPE!

1 21 1180 13 X APPROXIMATE TANDEM REPE!

1 21 286 A (TYPE I).

AT 287 358 B (TYPE II).
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SHLTIGTVAEINIGAGNLFTIDASVG 1266
                                                 GSLAANNIDFGARSTLEFNGPLDGG-----GKAIPYYFKGAIANGNNAILNVNTKLLTA
                                                                                                  VVVTGAIDNTG-----
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                         -----GTASGNSRGH---FGASASVG
                                                                           KSMMA-----
                                                                                                                          GVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARA----
                                                                                                                                                VTGNVGN-----
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                                                                                                  -NANNGIVTFTGNSTVTGDIGNTNALATVNVGAGITLQA---G
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AC Q9KKA3; Q9KK98; Q9XC45;

AC Q9KKA3; Q9KK98; Q9XC45;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-FEB-2003 (Rel. 41, Last annotation update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Outer membrane protein B precursor (168 kDa surface-layer protein)

DE (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rompB)

E (romp B) (Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
                                                        Rickettsiaceae;
NCBI_TaxID=781;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The rickettsial outer membrane protein A and B genes of Ricket australis, the most divergent rickettsia of the spotted fever submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETISIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
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gene coding the
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Samson D., Roux
Raoult D.;
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MEDLINE=21442074; PubMed=11557893;
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                                                                                                                                        SEQUENCE
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3L; AF123721; AAF34124.1; -.
3L; AF123726; AAF34129.1; -.
3L; AF149110; AAD39533.1; -.
3; E97835; E97835.
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32 KDA BETA PEPTIDE.

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P33666; P76087; P76088; P76856; P76857
01-FEB-1994 (Rel. 28, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Hypothetical protein ydba.
                                                                                                                                                                                                                                                            Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Sampei G., Seki Y., Siyasundaram S., Tagami H., Takeda J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
MEDLINE=92190338; PubMed=1665988;
Moszer I., Glaser P., Danchin A.;
"Multiple IS insertion sequences
                                                                                                                                                       corresponding to the 28.0-40.1 DNA Res. 3:363-377(1996).
                                                                                                                                                                                                           Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,
Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T
"A 570-kb DNA sequence of the Escherichia coli K-12 genome
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97251357; PubMed=9097039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete genome sequence 177:1453-1474(1997).
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-!- CAUTION:
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schimie 73:1361-1374(1991).

schimie 73:1361-1374(1991).

reflice 73:1361-1374(1991).

THIS IS A CONCEPTUAL TRANSLATION;

THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2
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L; AE000237; AAC74487.1; ALT_SEQ.
L; D90778; BAA15099.1; ALT_SEQ.
L; D90778; BAA1880.1; ALT_SEQ.
L; D90779; BAA1881.1; ALT_SEQ.
L; X62680; NOT_ANNOTATED_CDS.
Sene; EG11307; ydbA.
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InterPro; IPR005546; Autotransporter.
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PIR; S07575; S07575.
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-i- FUNCTION: MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Alp
Rickettsiaceae; Rickettsieae;
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                             CARBOHYD
                                              CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGRFAMs;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION. SUBSCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.
MISCELLANEOUS: ITS C-TERMINUS POTENTIALLY MAY BEAR THE EPITOPES CONFERRING ANTIGENICITY TO THE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way lifed and this statement is not removed. Usage by and for commercial tites requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
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Glycoprotein; Cell wall; S-layer
                             CAA34402.1;
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                                                           1211
              132801
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ed protein.
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"Cloning, expression and sequence analysis of the 120 kD surface-exposed protein of Rickettsia ricke Mol. Microbiol. 3:1579-1586(1989).

-i- FUNCTION: THE 120 kDa SURRACE-EXPOSED PROTEIN STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFEC
                                                                                                                                                                                                                       MEDLINE=90136087; PubMed=2515418; Gilmore R.D. Jr., Joste N., McDonald G.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92167802; pubMed=1724278;
Gilmore R.D. Jr., Cieplak W. Jr., Policastro P.F., Hackstadt T.;
"The 120 kilodalton outer membrane protein (rOmp B) of Rickettsia
rickettsii is encoded by an unusually long open reading frame:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
Rickettsiaceae; Rickettsi
                                                                                                                                                                                                                                                                                                 STRAIN=R;
                                                                                                                                                                                                                                                                                                                                                                                                                                          evidence for
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ol. 5:2361-2370(1991).
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  (Cell surface antigen 5) (Sca5) (rOmpB)
Da surface-exposed protein (Surface prote
embrane protein ompB); 32 kDa beta peptid
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RESULT FLIC\_SH ID FLIC AC 00 DT 01 DT 01 DT 28 DE F1 GN F1 OS S1 OC B6

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FLIC\_SHIFL STAN Q08860; Q1-NOV-1995 (Rel. 3 Q1-NOV-1995 (Rel. 3 Q1-NOV-1995 (Rel. 3 Q8-FEB-2003 (Rel. 4 Flagellin FLIC OR SF1966. Shigella flexneri.

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Enterobacteriaceae; Bacteria; Proteobacteria;

Shigella

Gammaproteobacteria;

Enterobacteriales;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X16353; CAA34403.1; -. FIR; S18227; S18227. InterPro; IPR006315; Autotransport. InterPro; IPR005546; Autotransporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a or send an email to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAYER WITH HEXAGONAL SYMMETRY.
-!- SIMILARITY: BELONGS TO THE RICKETTSIAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
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an email to license@isb-sib.ch).
                                                                                                               RNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVRIT----
                                                                                                                                                                                                                                                                     GLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVT-SGTNVTFASG-----KGTT
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                                                                                                                                                                                                                                                                                                                      --VESKDNG-----KKTEVKIGAKTSVIKEKDGKLVTGKDK-----
                                                                                                                                                                                                                                                                                                                                                                       NRAASVK--DVLNAGWNIKG--VKPGTTASDNVDFVRTYD---TVEFLSADTKTTTVN--
FNGNTTIAAN-STLQIGGNYTADCVASADGTG
                        YRGEAGYAIGYSSISDGGNWIIKGTASGNSRG
                                                VFNAGGTNIVS-GTVGGQQGNKFNTV-
                                                             VKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGT
                                                                                                                                               SSKTVLSNGNVAINELVIGNDGAVQFAHDTYLITRTTNAAGQGKIIFNPVVNNGTTLAA-
                                                                                                                                                                      SSGKVIS-GNV-----
                                                                                                                                                                                                IKLT-STQNNIVVDFDLAIATDQTGVVDASSLTNAQTLTINGKIGTIGANNKTLGQFNIG
                                                                                                                                                                                                                      ATVSKDDQGNITVMYDV-----NVGDALNVNQLQNSGWN-----LDSKAVA----G
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32 kDa BE
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SEQUENCE
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-!- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES FORM THE FILAMENTS OF BACTERIAL FLAGELLA.
-!- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dc
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tominaga A., Mahmoud M.A.-H., Mukaihara T., Enomoto "Molecular characterization of intact, but cryptic, in the genus Shigella.";
                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00700; Flagellin_C; Pfam; PF00669; Flagellin_N; PRINTS; PR00207; FLAGELLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D16819; BAA04093.1; -. EMBL; AE015215; AAN43516.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22272406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol. Microbiol. 12:277-285(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001492; FlagellinN
                                                                                                                                                                                                                                                                                                                                                                                                 PIR; S44980; S44980.
InterPro; IPR001029; Flagellin_C.
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sen the Swiss Institute of Bioinformatics and the EM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                  Similarity
                      QISSDGKITASNGDKLYIDTTGRLTKNGS----
                                                                  ASATNYKYDSASKSYSFDTTTASAADVQKYLTPG
                                                                                                           GAVANTAASKADLVAANATVVGNKYTVSAGYDAAKASDLLAGVSDGDTVQATINNGFGTA
                                                                                                                                                      DEIDRYSGQTQFNGVNYLAKDGSMK---IQYGANDGQTITIDLKKIDSDTLGLNGFNYNGG
                                                                                                                                                                                                LTQAARNANDGISVAQTTEGALSEINNNLQRIRELTVQASTGTNSDSDLDSIQDEIKSRL
                                                                                                                                                                                                                                                                VSELTRNHTKRASATVKTAV--LATLL-----FATVQASANRAASVKDVLNAGWNIKG
 ALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNN---
                                            KGKMDETVNINAGNNI - - - - -
                                                                                    ATVS--KDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGK---VISGNVSPS
                                                                                                                                EGL---VTAKEVIDAVNKAGWRMKTTTANGQTG--QADKFETVTSGTNV--TFASGKGTT
                                                                                                                                                                           DTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEG
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                                                                                                                                                                                                                                                                                                                                  56636 MW;
                                                                                                                                                                                                                     -----KPGTTASDNVDFVR----TY
                                                                                                                                                                                                                                                                                        68;
                                                                                                                                                                                                                                                                                                 Score 148;
Pred. No. 0.
                                          -EITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD
                                                                                                                                                                                                                                                                                                                                  CC921C9A8EF200B6 CRC64;
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.27;
                      -GASLTEASLSTLAANNTKATTIDIGGT
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                                                                                                                                                                                                                                                                                      183;
                                                                 -----VGDTAKGTITIDGSAQDV
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flagellin
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RESULT 10
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EMBL; U01028; AAA17405.1; EMBL; AE008674; AAL03811... EMBL; U43794; AAB49549.1;
                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See
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16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
28-FEB-2003 (Rel. 41,
                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                              STRAIN-Indian tick typhus, M1, Malish 7, and Moroccan; Raoult D., Fournier P.E., Roux V.; "Phylogenetic analysis of spotted fever group rickettsiae of the outer surface protein rOmpA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiffren
Samson D., Roux V., Cossart P., Weisse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Crocquet-Valdes P.A., Weiss K., Walker D.H.; "Sequence analysis of the 190-kDa antigen-encoding conorii (Malish 7 strain)."; Gene 140:115-119(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiaceae; Rickettsieae; Rickettsia.
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OMPA OR RC1273.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE
                                                                                                                                                                                                                                               the outer surface protein rOmpA.";
bmitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
- FUNCTION: ELICITS PROTECTIVE IMMUNITY (BY SIMILARITY)
- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COS-LAYER WITH HEXAGONAL SYMMETRY.
- PTM: GLYCOSYLATED (BY SIMILARITY).
                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY
                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EM
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                                                                         s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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; U43806; AAB49551.1;
; U45244; AAB49566.1;
; U46918; AAAB6663.1;
; U46918; AAAB6663.1;
; U83440; AAC35176.1;
; U83443; AAC35179.1;
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; TIGR01414; autotrans_barl;
Repeat; Signal; Cell wall;
                                                                              KIGAKTSVIKEKDGKLVTG----KDKGENGSSTDEGEGLVTAK----EVIDAVNKA----
                                                                                                                                            WNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTT----TVNV---
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N -> NN (IN STRAIN INDIAN TICK TYPHUS).

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MISSING (IN STRAIN M1).

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VT -> II (IN STRAIN INDIAN TICK TYPHUS).

D -> A (IN STRAINS INDIAN TICK TYPHUS, M1
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SLAP_CAUCR STANDARD; PRT; 1025 AA.
ID SLAP_CAUCR STANDARD; PRT; 1025 AA.
AC P35828; Q46015; Q9FFI2;
DT 01-JUN-1994 (Rel. 29, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE S-layer protein (Paracrystalline surface layer
GN RSAA OR CC1007
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=ATCC 19089 / CB15;

STRAIN=ATCC 19089 / CB15;

NIETMAN M.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Nierman M.C., Feldblyum T.V., Laub M.R.K., Ohta N., Maddock J.R., Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Phadke N.D., Ely B.

POTOCKA I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.

POTOCKA I., Nelson W.C., Durkin A.S., Gwinn M.L., Haft D.H., Ely B.

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven.M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White
                                                                                                                                                                                                                                                                                                                                                                                                    REVISIONS Awram P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 1-21; STRAIR-ATCC 19089 / CB15; MEDLINE-93007489; PubMed-1393820; MILCHRIST A., Fisher J.A., Smit J.K.; Nucleotide sequence analysis of the generoscentus paracrystalline surface layer cap. J. Microbiol. 38:193-202(1992).
                                                                                                                                                                                                                                                                                    Bingle
"The se
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-JS3001;
Bingle W.H., Awram
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Caulobacteraceae; Caulobac
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                                                                                                                                                                                                                                               gle W.H., Awram P.A., Nomellini J.F., Smit J.K.;
e secretion signal of C. crescents S-layer protein
C-terminal 82 amino acids of the molecule.";
mitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
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J. Bacteriol. 170:4706-4713(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
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STRAIN-ATCC 19089
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Proc. Natl. Acad. Sci. U.S
                                                                                                                                                                                                                                                                                               PRINTS;
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AF193063; AAF19365.1;
AE005779; AAK22991.1;
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LTLNVNGLTTTGAITDSEAAADDGFTTINIAGSTASSTIASLVAADATTLNISGDARVTI
                                           AASATTAGKIATVTLGSFGAATIDSSALTTVNL-SGTGTSLGIGR----GALTATPTANT-
                                                                                     TAGNAVNTTLTQADVTVTGNSSTTAVTVTQTAAATAGATVAGRVNGAVT-----ITDSA
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U.S.A. 98:4136-4141(2001).
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                                                                                                          - EGLVTAKEVIDAVNKAGWRMKTTTA
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Matuschek M., Burchhardt G., Sahm K., Bahl H.;
Matuschek M., Burchhardt G., Sahm K., Bahl H.;

"pullulanase of Thermoanaerobacterium thermosulfurigenes EM1
(Clostridium thermosulfurogenes): molecular analysis of the gene,
composite structure of the enzyme, and a common model for its
attachment to the cell surface.";

J. Bacteriol. 176:325-3302(1994).

-i- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
linkages in oligosaccharides and polysaccharides.

-i- CATALYTIC ACTIVITY: Hydrolysis of (1-5)-alpha-D-glucosidic
-i- CATALYTIC ACTIVITY: Hydrolysis of (1-5)-alpha-D-glucosidic
Pfam; PF00128; alpha-amylase; Pfam; PF02806; alpha-amylase_refam; PF02903; alpha-amylase_refam;
                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=DSM 3896 / MEDLINE=94252998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thermosulfurogenes).
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1994 (Rel.
01-NOV-1995 (Rel.
28-FEB-2003 (Rel.
                                                                                       InterPro; IPR006589; Alp_amyl_cat_sub.
InterPro; IPR006048; Alpha_amyl_C.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR008161; FN_III.
InterPro; IPR008185; Glyco_hydro_13IG.
InterPro; IPR008185; Glyco_hydro_13N.
InterPro; IPR008119; SLH.
                                                                                                                                                                                                                                                                                               EMBL; M57692;
HSSP; Q08751;
                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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SIMILARITY: Contains 3 S-layer homology (SLH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute.
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Kuwajima G., Asaka J.-I., Fujiwara "Nucleotide sequence of the hag gen Escherichia coli.";
J. Barteria
                                    Wilkins M.R., Gasteiger E., Tonella L., Ou K., Tyler M., Sanchez J.-C., Gooley A.A., Walsh B.J., Bairoch A., Appel Williams K.L., Hochstrasser D.F.;
"Protein identification with N and C-terminal sequence tag proteome projects.";
J. Mol. Biol. 278:599-608(1998).
-!- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYM FORM THE FILAMENTS OF BACTERIAL FLAGELLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97251358; PubMed=9097040; Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura Makade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.; A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage mal DNA Res. 3:379-392(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blattner F.R., Piunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
    This
                                                                                                                                                                                                                                                                                                                           Link A.J., Robison K., Church G.M.; "Comparing the predicted and observed Fin the genome of Escherichia coli K-12. Electrophoresis 18:1259-1313(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=83238225;
Szekely E., Simon
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Hanafusa T., Sakai A., Tominaga A.,
"Isolation and characterization of
                                                                                                                                                                                                                                       STRAIN=K12 / W3110;
MEDLINE=98263247; PubMed=9600841;
                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=K12 / EMG2;
MEDLINE=97443975; PubMed=9298646;
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SWISS-2DPAGE; P04949; COLI.
ECOGENE, EG10321; flic.
InterPro; IPR001029; Flagellin_C.
InterPro; IPR001492; Flagellin.C.
Pfam; PF00700; Flagellin_C; 1.
Pfam; PF00669; Flagellin_N; 1.
PRINTS; PR00207; FLAGELLIN.
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 Y741_CHLMU
Q9PJT6;
16-OCT-2001
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97; Conser
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                                                                                                                     AYLPGKSMMA 384
                                                                                                                                            ASVDKFRSSLGAVQN--RLDSAVTNLNNTTTNL-SEAQSRIQDADYATEVSNMSKAQIIQ
                                                                                                                                                                    GVKE-----GDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQA-----IATAGLVQ
                                                                                                                                                                                            VKLGGDDGKTEVVDIDGKTYDSADLNGGNLQTGLTAGGEALTAVANGKTTDPLKALDDAI
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Last seq
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PIR; H81670; H8:
TIGR; TC0741; -
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113; Conserv
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             ETVVSPYRGGGGNTSSPIGLA-SLLPATPSTPLMTTPRTNGKAAASSLMIKGGETQA---
                                                                                                                                                          GKTTSTEENGDPSGPDILAAVRKHLDTVYPGENGGSTEGPL--PANQNLGNVIHDVEQNG
                                                                                                                                                                                                                           ANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNS
                                                                                                                                                                                                                                                                                                     DTSDIDTNNQTNGDINTNDNSNNVDGSLSDVDSRVEDDDGVSDTESTNGNDSGKTTSTEE
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                                                          PVGDGGTPSGPDILAAVRKHLDTVYPGENGGSTERPLPAN---QNLGDIIHDVEQNGSAK
                                                                                                          AAQE -- TIITPGDTESTDTSSSVNANADLEDVSDADSGFGDDDGISDTESTNGNDSGKNT
                                                                                                                                 KNIDIATSMTP----QFSSVSLGAGADAPTLS-----
                                                                                                                                                                                                       TPGDTGPTDSSSSVDADADVEDTS - DTDSGIGDDD - - - - - - - GVSDTESTNG - NNS
                                                                                                                                                                                                                                                     NGDPSGPDILAAVRKHLDTVYPGENGGST---EGPLPANQNLGNVIHDVEQNGSAKETII
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1007
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                                    -RAGIAQAIATAGLVQAYLP---
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----GENGSSTDEGEGLVTAKE----VIDAVNKAGWRMKTTT

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276

-SGNVSPSKGKMDETVNINAGNNI-EITRNG

---VDGDALNVGSKKDNK

319 686

-RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNA---

359 744

-----GK----SMMAIGGGTYRGEA

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16-OCT-2001 (Rel. 40, L
Hypothetical protein TC
TC0741.
Chlamydia muridarum.
Bacteria; Chlamydiae; (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R. Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                     Hypothetical protein; SIGNAL 1 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequences of pneumoniae AR39."; Nucleic Acids Res. 28
                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                       44 FATVQASANRAASVKDVLNAGWNIKGVK------PGT-TASDNVDFVRTYDTVEF
                                               FATPPSSPSQT----PVINVNVNVGGTNVNIGDTNVSKGSGTPTSSQSVDM--STDTSDL
                                                                                                                                         Conservative
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CRC64;
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RESULT 15

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CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA REQUIRES SHLB FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Bacteriol. 170:3177-3188(1988).
-I- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-SN8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 31-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serratia marcescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hemolysin precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hemolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Poole K., Schiebel E., Braun V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=88257037; PubMed=3290200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterobacteriaceae; Serratia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINED.
                                                                                                                                                                                                                                                                                                             717
                                                                                                                                                                                                                                767 --KVSFLAADDKTAS-NTE-----QTKIGG-----
                                                                                                                                                                                                                                                                86 YDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDE 145
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                                                                                                            DOGNITYMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 265
                                                                                                                                                                                                                                                                                                           AGNNIEITRNGKNIDIATSMTPQFSSVSLGA------GADAPTLSVDGDALNVG
                                                                          -KGNLT----INARDKLTQQGAQHSVGGAYQENAAGVDHLAAADTASTTTTKTDVGVNI-
                                                                                                                                                      -----GIDKLGSGVEAGYENNKT-QAQSSKAITSGSDV-----
                                                                                                                                                                                          GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 205
                                                                                                                                                                                                                                                                                                                                   HTKRASATVKTAVLATLLFATVQASANRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRT
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1608 AA; 165078 MW; D669B476FE7DAD51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Toxin; Outer membrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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-GANVDYSAVTRPVERAVGKAAKLDATGVINDIGGIGAPNVGLDIGAQGGS 930
                                                                                                                                                                                                                                                                                                                                                                                   6.5%; Score 142; DB 21.9%; Pred. No. 2; tive 53; Mismatches
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Db	Qy	DЪ	Qy	DЪ	Qy
1042 INVNVKKDA	2y 410IKGTASGNSRGHFGASA 427	990 EQSRDTRGSAG-VRVYTTTGSDLTVDAKGEGGTQRSNSSASQAVTGSIDAANG 1041	354 NVDGNA	931	29 314 SKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRID 353
		rgsidaang 1	SSISDGGNW 4	SEAAANRQD 9	NRID 3
		041	601	989	153

Search completed: October 6, 2003, 09:24:03 Job time: 9.68663 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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    2108
2108
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1: sp_archea:*
2: sp_bacteria:
3: sp_fungi:*
4: sp_human:*
5: sp_invertebb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel1:
9: sp_phage:*
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Gapop 10.0 , Gapext 0.5
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301.5	315.5	315.5	326	326	328	329.5	335	340.5	355.5	382	489.5	509.5	655.5	664.5		734	775.5	776.5	1920	1920	1964	1976	1981.5	1998	2001.5	2005.5	2006	2009.5
13.7	14.4	14.4	14.8	14.8	14.9	15.0	15.2		16.2	7.	•	23.2	29.8	30.2	31.3	•	35.3	35.3	87.4	87.4	89.4	•	90.2	90.9	91.1		91.3	91.5
2712	658	641	1778	1107	1461	1588	1190	2059	2314	1299	1002	1004	1210	1210	1204	2353	1096	1098	530	526	589	589	600	599	598	598	595	592
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Q9F3X5	Q8ZHJ0	Q8CKM1	Q8FCB2	Q9F2D8	Q8ZL64	Q8XDG4	Q9PC04	Q9PD50	Q8KQM8	Q9F3X6	Q8GM78	Q8GM77	Q8GM75	Q8GM74	Q8GM76	P71401	Q8GM79	048152	Q9JPS1	Q9JPS4	Q93QY1	Q9JPI0	Q9JPS5	Q9JPS8	Q93QY5	Q9JPR7	Q9JРН0	Q9JQW4
Q9f3x5 pasteurella	yersinia	Q8ckm1 yersinia pe	Q8fcb2 escherichia	Q9f2d8 salmonella	Q8z164 salmonella	Q8xdg4 escherichia		Q9pd50 xylella fas		6		7				P71401 haemophilus		Q48152 haemophilus		Q9jps4 neisseria m	Q93qy1 neisseria m	_	Q9jps5 neisseria m	Q9jps8 neisseria m	Q93qy5 neisseria m	Q9jpr7 neisseria m	Q9jphO neisseria m	Q9jqw4 neisseria m

## ALIGNMENTS

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Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,	, Fleischmann K.D., Dougnerty		Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,	Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,	MEDLINE-20175755; PubMed-10710307;	STRAIN-MC58 / Serogroup B;	SEQUENCE FROM N.A.		Science 287:1816-1820(2000).		"Identification of Vaccine Candidates Against Serogroup B	Moxon E.R., Grandi G., Rappuoli R.;	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,		Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,	Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,	Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,	MEDLINE=20175756; PubMed=10710308;	STRAIN=MC58 / Serogroup B, BZ169, BZ83, and H44/76;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=487, 491;	Neisseriaceae; Neisseria.		Neisseria meningitidis (serogroup B).	Neisseria meningitidis, and	GNA992 OR NMB0992 OR NHHA.		GNA99	(TrEMBLrel. 22, Last		01-OCT-2000 (TrEMBLrel. 15, Created)	••	Q9JR18 PRELIMINARY; PRT; 591 AA.	œ	AT 1

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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=N.meningitidis; STRAIN=PMC21; Peak I.R., Srikhanta Y., Dieckelman M
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L; AF226375; AAF42524.1; -.

L; AF206367; AAF42516.1; -.

L; AF226367; AAF42516.1; -.

L; AF226370; AAF42519.1; -.

L; AF226370; AAF42519.1; -.

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al Similarity 73.3%;
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E 591 AA; 6
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| MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL
                                                                                                                                       MAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
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ARDLINE-20175756; PubMed=107105756; ARP42515-1;
ARDLINE-2017576; PubMed=107105754; PubMed=107105
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Outer membrane protein GNA992.
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                                                                           SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
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STRAIN-MC58:
Peak I.R., Srikhanta Y., Dieckelman M., Moxon E.R.
Identification and characterisation of a gene enc
membrane protein of Neisseria meningitidis.";
L Submitted (FEB-1999) to the EMBL/GenBank/DDBJ datu
EMBL; AF125375; AAK09243.1; -
EMBL; AF125375; AAK09243.1; -
InterPro; IPR005594; YadA.
R InterPro; IPR005594; YadA,
R Pfam; PF03895; YadA; 62290 MW; 168986A97381EFC5 C
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Q9AQFO;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2002 (TrEMBLrel. 22,
Outer membrane protein.
NHHA,
Neisseria meningitidis.
Bacteria; Proteobacteria; B
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Bacteria; Proteobacteria;
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"Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
EMBL, AF226371; AAF42520.1;
TINTERDERGAL YSSA.
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NCBI_TaxID=487;
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         QAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGY
                                    SKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLV
                                                                                        SKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVG
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                                                                            SKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVG
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3895; YadA; 1.
600 AA; 62762 MW;
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Deae; Neisseria.
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A Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
A Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
A Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.
A Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti
A Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.
A Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
A Hood D.W., Jeffies A.C., Saunders N.J., Granoff D.M., Venter C.
A Moxon E.R., Grandi G., Rappuoli R.;
"Identification of Vaccine Candidates Against Serogroup B
"Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
R EMBL; AF226361; AAF42510.1; -.
R InterPro, IPR005594; YadA.
R Pfam; pF03895; YadA; 61917 MW; 4A3471514FD3C879 CRC64;
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GNA992.
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Bacteria; Proteobacteria;
Neisseriaceae; Neisseria.
NCBI_TaxID=487;
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                                               RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKS
                                                                                                             NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDG-DALNVGSKKDNKPV
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. 15, Last sequence update)
. 22, Last annotation update
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: Pred. No. 3e-8
1; Mismatches
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WEDLINE-20175756; PubMed-10710308;

WEDLINE-20175756; PubMed-10710308;

A Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,

RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

RA Moxon E.R., Grandi G., Rappuoli R.;

"Identification of Vaccine Candidates Against Serogroup B

Meningococcus by Whole-Genome Sequencing.";

REL Science 287:1816-1820(2000).

RMBL; AF226378; AAF42527.1;

Therefore, Ternongsal. Vala.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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NCBI_TaxID=487;
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3895; YadA; 1.
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ceae; Neisseria.
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71.5%;
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Pred. No. 1.26
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Best Local S
Matches 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Meningococcus by Whole-Genome Sequencing Science 287:1816-1820(2000).
EMBL; AF226379; AAF425281; -.
InterPro; IPR005594; YadA.
Pfam; PF03895; YadA; 1.
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MEDLINE=20175756; PubMed=10710308;
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NCBI_TaxID=487;
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                                                                  TVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE
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 TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANK
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Pred. No. 1.6e-86;
1; Mismatches 10;
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Betaproteobacteria; Neisseriales;
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Pfam; PF03
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3895; YadA; 1.
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(TrEMBLrel. 22,
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O1-OCT-2002 (TrEMBLrel. 2
Outer membrane protein GN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peak I.R., Srikhanta Y., Dieckelman M., Moxon "Identification and characterization of a genemembrane protein of Neisseria meningitidis."; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=H38;
Peak I.R., Srikhanta Y.,
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NCBI_TaxID=487;
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                                             EPVVRSALVLQFMIDKEGNGENESTGNIGWSIYYDNHNTLHGATVTLKAGDNLKIKQNTN
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                                                                                                                                               DTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDKKKRAASVKDVLNAGWNIKGVKPGTT
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A Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
A Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,
A Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
A Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
A Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
A Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
A Moxon E.R., Grandi G., Rappuoli R.,
T "Identification of Vaccine Candidates Against Serogroup B
"Identification of Vaccine Sequencing.";
Science 287:1816-1820(2000).
Science 287:1816-1820(2000).
R EMBL, AF226369; AAF4255.1; -.
R EMBL; AF236369; AAF42518.1; -.
R InterPro, IPR005594; YadA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=NG3/88, and BZ232;
MEDLINE=20175756; PubMed=10710308;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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DFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENG
                                       LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV
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                                                                                                                                                                   Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jei "Identification and characterization of a gene encod membrane protein of Neisseria meningitidis "; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databa: EMBL; AF226388; AAF42517.1; -. EMBL; AF226388; AAF42507.1; -. EMBL; AF157604; AAK68865.1; -. EMBL; AF157604; AAK68865.1; -. InterPro; IPRO05594; YadA. Pfam; PF03895; YadA; 1. Pfam; PF03895; YadA; 1.
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01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-CCT-2002 (TrEMBLrel. 22, Last annotation update)
01ter membrane protein GNA992 (NhhA outer membrane GNA992 OR NHHA.
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STRAIN-BZ198, and 297-0;

MEDLINE-20175756; PubMed-10710308;

MEDLINE-20175756; PubMed-10710308;

Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico'

Comanducci M., Jennings G.T., Baldi L., Bartolini E., Cape

Caleotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M.

Ratti G., Santini L., Savino S., Scarselli M., Storni E.,

Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettel

Hood D.W., Jeffries A.C., Sannders N.J., Granoff D.M., Ven

MCYON F B. Grandi G. Pannoli P.
                                                                                                                                                                                                                                                                                                                                                                                                                     Moxon E.R., Grandi G., Rappuoli R.; "Identification of Vaccine Candidates Against Meningococus by Whole-Genome Sequencing."; Science 287:1816-1820(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis.
Bacteria; Proteobacteria;
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NCBI_TaxID=487;
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                                                                                           Score 2025.5; DB 2
Pred. No. 3.8e-86;
2; Mismatches 10;
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Matches Query Match Best Local

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                                               Meningococcus by Whole-Genome Science 287:1816-1820(2000).
EMBL; AF226382; AAR42531.1;
InterPro; IPR005594; Yada.
Pfam; PF03895; Yada; 1.
                                                                                 Broeker M., Hundt E., NHUPP J., Grano Hood D.W., Jeffries A.C., Saunders N.J., Grano Moxon E.R., Grandi G., Rappuoli R.;
"Identification of Vaccine Candidates Against "Identification of Vaccine Candidates Against ""
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Q9JPR9;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation updato)
Outer membrane protein GNA992.
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Bacteria; Proteobacteria;
Neisseriaceae; Neisseria.
                                           SEQUENCE
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Pred. No. 4.8e-86;
2; Mismatches 10
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Q93QY2;
Q1-DEC-2001
Q1-DEC-2001
Q1-OCT-2002
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Bacteria;
                                                                                                  Peak I.R., Srikhanta Y., Dieckelman M., Moxon R "Identification and characterization of a gene membrane protein of Neisseria meningitidis."; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ d EMBL; AF157609; AAK68870.1; -. InterPro; IPRO05594; YadA.
                                                                                                                                                                                                       Neisseria meningitidis.
Bacteria; Proteobacteria;
Neisseriaceae; Neisseria.
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                                                                                          InterPro; IPRO
Pfam; PF03895;
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YLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
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protein.
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Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecch
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Moxon E.R., Grandi G., Rappuoli R.;
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Science 287:1816-1820(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9JPSO, PRELIMINARY; PRT; 598 AA.
Q9JPSO;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation updat outer membrane protein GNA992 (NhhA outer membran GNA992 OR NHHA.
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Bacteria; Proteobacteria;
Neisseriaceae; Neisseria.
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NCBI_TaxID=487;
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Дb	Оy	Оу Оъ	Qу	Qу Дъ	Оу	. pb Qy	Db	Qy Qy	γQ	Qу Дъ	Ма	DR DR DR
376 YLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSNGHFGASASVGYQW 433 		257 KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSK 315 	197 GTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKG 256 	137 GENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGK 196 	77 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLYTGKDK 136 	52	121 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGD 180	61 PVQRTAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE 120	52 51	1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASA 51	Query Match 91.5%; Score 2010.5; DB 2; Length 598; Best Local Similarity 69.9%; Pred. No. 1.9e-85; Matches 418; Conservative 3; Mismatches 12; Indels 165; Gaps 2;	EMBL; AF157607; AAK68868.1; InterPro; IPR005594; YadA. Pfam; PF03895; YadA; 1. SEQUENCE 598 AA; 62763 MW; E6C7AEF0BB8A63CB CRC64;

Search completed: October Job time: 34.8023 secs 6 09:30:42

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Result
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A surface protein
N. meningitidis PM
A surface protein
BASB029 amino acid
A surface protein
N. meningitidis EG
N. meningitidis PM
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M. catarrhalis les	AAB69136	22	2314	4.	372.5	45
-	ABP71294	24	2139		374	44
	AAE30477	24	298		523.5	43
	AAB23859	21	1104	ω	594	42
Haemophilus influe	AAB23856	21	1104	ω.	594	41
C	AAB37832	21	116	ω	600	40
Haemophilus influe	AAB23854	21	1002	6.	661	39
Haemophilus influe	AAB23857	21	1004	26.8	682	38
ຜ	AAY27201	20	245	7.	690.5	37
	AAB23855	21	679	ω	847.5	36
	AAR99394	17	679	ω.	847.5	35
	AAB23858	21	1094	5	906	34
	AAR99392	17	1098	8	974	$\omega$
	AAR99393	17	2353	9.	1009.5	32
Haemophilus influe	AAB23860	21	2411	9.	1011.5	31
N. meningitidis PM	AAU06184	22	407	8.	2005.5	30
N. meningitidis PM	AAU06185	22	433	2	2098.5	29
	AAU06181	22	604	5	2166	28
N. meningitidis H4	AAU06183	22	513	8	2255.5	27
N. meningitidis P2	AAU06173	22	589	Ξ.	2317.5	26
A surface protein	AAY23745	20	589	1.	2317.5	25
Amino acid sequenc	AAY27203	20	592	<u> </u>	2323	24
	AAU06172	22	592	1.	2327	23
	AAY23744	20	592		2327	22
N. meningitidis BZ	AAU06178	22	598	1	2335	21
	AAY23738	20	598	۲.	2335	20
itidis	AAU06177	22	598	2	2344	19
ř	AAY23742	20	598	2	2344	18
	AAU06180	22	592	2	2351	17
itidis	517	22	594	92.7	2359	16
surface prote	AAY23739	20	594	2	2359	15
N. meningitidis EG	AAU06174	22	594	ω.	2366	14
	704	21	594	ω	2366	13
surface protei	AAY23740	20	594	ω.	2366	12
itidis	51	22	599	93.2	2371.5	11
A surface protein	AAY23743	20	599	ω.	2371.5	10

## ALIGNMENTS

AAU06186 standard; Protein; 502

A

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RESULT 1
AAUU6186
IID AAUU6186
AC AAUU6
XX N. m
AC AAUU6
AC N. m
XX Neis
XX Neis
XX Neis
XX Neis
XX Pep Prot
FT Porot
FT Prot
FT Prot
FT Prot
FT Prot
XX No 25-J
PR AUG1886
                                                                                                                                                                                                                                                  Surface antigen NhhA; meningococcal disease; meningitis vaccine; mutant; mutein.
                                                                                                                                                                                                                                                                                        N. meningitidis PMC21 NhhA deletion mutant #4
             25-JAN-2000; 2000US-0177917
                                                             02-AUG-2001.
                                                                                     WO200155182-A1.
                                                                                                                                                   Protein
                                                                                                                                                                           Peptide
                                                                                                                                                                                                               Neisseria meningitidis strain PMC21. Synthetic.
                                                                                                                                                                                                                                                                                                               24-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                        AAU06186;
                                    25-JAN-2001; 2001WO-AU00069
                                                                                                            /label= Signal_peptide
50..502
50..502
/label= Mature_NhhA_deletion_mutant_#4
/note= "Predicted mature protein, specifically
claimed in claim 12"
                                                                                                                                                                                       Location/Qualifiers
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ORF40-1 vaccine;

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RESULT 2
AAY27202
ID AAY2
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhha (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively inmunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence represents N. meningitidis strain pMC21 surface antigen NhhA deletion mutant #4.
                AAY27202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                481
                                                                                                         481
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B; AAS09176.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                    GIGSTLTDRAASVKDVLNAGWNIKGVKNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KGTASGNSRGHFGASASVGYQW
                                                                                                                                TEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   KIKQFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIKQFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN
               standard;
                                                                                KGTASGNSRGHFGASASVGYQW
                                                                                                                                                                                                                                        WNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSS
                                                                                                                                                                                                                                                       WNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSS
                                                                                                                                                                                                                                                                                                                                                                                                  GIGSTLTDRAASVKDVLNAGWNIKGVKNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fig 9; 91pp;
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               Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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               591
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Pred. No. 1.9e-152;
Mismatches 0;
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                                                                                502
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Best Local S
Matches 502
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14-JAN-1998;
01-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                        The invention provides proteins (AAY27201-245) from Neisseria meningitidis (Strains A and B) and nucleic acid sequences (AAX99123-1 encoding the proteins. Compositions comprising the protein, nucleic a or antibody specific to the protein are useful as pharmaceuticals, evaccine composition or a diagnostic composition. The composition is a useful for treating or preventing an infection due to Neisserial bacteria, especially Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnostic co
meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria
bacterial
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09936544-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New protein and its nucleotide sequence, useful in vaccines diagnostic compositions for treating and/or preventing Neiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria
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DB; AAX99124.
  272
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                                                                                                                                                                                                                                                                                                                                               502;
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                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                          VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
                                                                                                                                   GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
                                                                                                                                                   GIGSTLTD-----
                                                                                                                                                                                                                                        YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 62;
                                                                               VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            meningitidis infection; to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence of N. meningitidis protein
                                                                                                                                                                                                                                                                                                                                                                                                  591
                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                  AA;
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98GB-0000760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
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                                                                                                                                                                                                                                                                                                                                                          96.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is protein; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English
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                                                                                                                                                                                                                                                                                                                                              Score 2459.5; DB Pred. No. 5e-147; 0; Mismatches
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DB 20; 0

Neisseria

or

(AAX99123-167)

e.g. acid

Indels Length

99;

Gaps

TLKAGDNLKIKQ

64

60

52

-NVDF

151

180 120 120

240

331

360

271 300 211

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RESULT 3
AAY23746
ID AAY27
XX AAY2
AC AAY2
XX AAY2
XX AY2
XX AY2
XX AY2
XX Neis
PN W099
PN W099
PN W099
PN U099
PN U14-F
XX 14-F
XX 14-F
XX 14-F
XX Neis
PT Ne
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                                                                                             Query Match
Best Local S
Matches 502
                                                                                                                                                                                       The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Surface protein; surface immunoreactive peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 127-128; 132pp;
                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis surface proteins useful for treating meningitidis infections
                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUN-1999
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                                                                                                                                                              Sequence
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                                                                                               Local Similarity es 502; Conserv
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DB; AAX85798.
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 53
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                              standard;
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                                                                                                                                                              591
                                                                                               Conservative
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                                                                                                          96.78;
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                                                                                             Score 2459.5; DB
Pred. No. 5e-147;
D; Mismatches (
                                                                                                                                                                                                                                                                                                                                                       English.
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                                                                                               0;
                                                                                                                             20;
                                                                                               Indels
                                                                                                                           Length
 -TLKAGDNLKIKQ
                                                                                                                             591;
                                                                                             ; 68
                                                                                                                                                                                                                                                       humans.
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                                                                                             Gaps
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 64
                               60
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AAU06171
ID AAU
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                                                                                                                                                                                                                                                                                                                                                                                       meningitidis strain PMC21
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                                                                                                                                                                                                                                                          /label= C1
/note= "Conserved region
51..108
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/label=_C3
 /note= "Conserved 189..210
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/note= "Variable
125..188
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Matches 502;
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                                                                                                                                                                                                                                                                                                                                                        The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhha (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen Nhha from N. meningitidis strain pMC21 is 1 of 10 Nhha polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; Fig 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
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VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
                                                                                                      MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASAN------
                                                    GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
                                                                                 GIGSTLTD---
                                                                                                                                                           YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ
                                                                                                                                                                                                                MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL
                                                                                                                                                                                                                                                                                                                         591 AA;
                                                                                                                                                                                                                                                                      Conservative
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/label=_(
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/note= "Variable region 3"
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/note= "Variable
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                                             meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Surface protein; surface glycoprotein; infection;
                                                                                                                                                                                                                                                                                                            Claim 1; Page
                                                                                                                                                                                                                                                                                                                                                              meningitidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunoreactive
                                                                                                                                                                                                                                                    present sequence represents a surface protein of Neiserria
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DB; AAX85788.
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                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IRA;
                                                                                                                                                                                                                                                                                                                                                                                      proteins
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Best Local Similarity Matches 501; Conserv

Conservative

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Score 2455; I Pred. No. 9.76 0; Mismatches

DB 20; .7e-147;

592; 90;

Indels Length

Gaps

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96.5%;

Query Match

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                                                                                                                                                                                                                                                                    amino acid sequence
                                                                                                                                                                                                                               Nisseria men:
n; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                        MMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q----FTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHL
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                                                                                                                                                                                                           meningitidis
                                                                                                                                                                                                                                                                                            (first entry)
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108
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92
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123
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                           /note=
389
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269
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                                                                                                                                                                                                                                meningitidis;
ent; prevent; ;
                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                            "Encoded
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antibacterial
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                                                                                                                                                                                                                                  drug.
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Matches 500
                                                                                                                                                                                                                                                                                                                                                                                                                polynucleotides and polypeptides are useful for generating an immune response in an animal. A therapeutic composition comprising an antibody directed against BASBO29 is useful in treating humans with Neisseria meningitidis disease. The polynucleotide is useful in the diagnosis of the stage of infection, type of infection, susceptibility to an infection which results from increased or decreased expression of the polynucleotide, and for therapeutic or prophylactic purposes, particularly genetic immunisation. Antibodies against BASBO29 polynucleotides and polypeptides are also useful for treating infections particularly bacterial infections. The protein is useful in the screening and development of antibacterial drugs. Fused recombinant protein is useful for the stimulation of the immune system of an organis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the Nisseria meningitidis BASB029 amino acid sequence from serogroup B strain H44/76. The BASB029 protein is homologous to the Haemophilus influenzae surface fibril (HSF) protein. The invention relates to BASB029 polynucleotide sequences (AAZ39864-Z39865) and polypeptide sequences (AAX57044-Y57045) and their immunogenic fragments. BASB029 polypeptides are useful in a method of diagnosing a Neisseria meningitidis infection in a mammal. Compositions containing BASB029
                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptide from neisseria meningitidis useful treatment or prevention of bacterial infections in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAY-1998;
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DB; AAZ39865.
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                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                  VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fig
SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
                                                 TDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
                                                                                                                                                                                 NGSNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN
                                                                                                                                                                                                                                                                                            MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASAN------
                                                                                                                                  GIGSTLIDTLLNIGATINVINDNVIDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
                                                                                                                                                                                                                                YLDPVQRTVAVLIVNSDKEGTGEKEKVEEDSNWAVYFDEKGVLTAREITLKAGDNLKIKQ
                                                                                                                                                                                                                                                                                 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL
                                    TDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
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84.6%;
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Pred. No. 1.4e-146;
                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                        Length
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                                                                                                                           The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                 Neisseria meningitidis surface meningitidis infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY23741 standard;
                                                                                                                                                                                                                             Claim 1; Page 104-106; 132pp;
                                                                                                                                                                                                                                                                                                             Jennings MP,
                                                                                                                                                                                                                                                                                                                                                                                14-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Surface protein; surface
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                                                                                                           Sequence
                                                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                                                (ISIS-)
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                                                                                                                                                                                                                                                                                                                                                                                                    24-JUN-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunoreactive peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          surface
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DB; AAX85793.
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                                      MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLEATVQASAN------
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                             MNEILRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM
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Pred.
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                                                                                                                                                                                                                                                                                                             IRA;
                                                                                                                                                                                                                                                           proteins useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         meningitidis.
                                                                     Mismatches
                                                                           2447.5;
No. 2.9e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection; vaccine,
                                                                            .9e-146;
                                                                                     BB
                                                                                                                                                                                                                                                           for
                                                                                       20;
                                                                                                                                                                                                                                                           treating
                                                                                     Length
          TLKAGDNLKIKQ
                                                                                        591;
                                                                    ; 88
                                                                                                                                                                     humans
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                                                                    Gaps
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RRESULT 8
AAU06175
AAU06175
AAU06175
AC AAU0
XX AAU0
DT 24-O
DX N. m
XX Surf
XX Surf
XX Regi
FT Regi
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                                                                                                                                                                                                                                                                                         N. meningitidis
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                                                                                                                              Region
                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                      Surface
                                                                                                                                                                                                                                                                                                             24-OCT-2001
                                                                                                                                                                                                                                                                                                                                AAU06175;
          Region
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                                                                                                                                                                                                                                                  Neisseria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                      antigen NhhA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIGSTLTD-------NVDF
                                                                                                                                                                                                                                                                                                                                                                                                                                        NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----FTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YLDPYLRTYAYLIYNSDKEGTGEKEKYEENSDWAYYFNEKGYLTAREITLKAGDNLKIKQ
                                                                                                                                                                                                                                                  meningitidis strain
                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                         EG329
         /note= "Conserved 230..236
                                                                                                /note= "Variable
125..188
                             /label= C4
                                                /label= V3
/note= "Variable
                                                                     189..210
                                                                                                                     /label=
                                                                                                                                       /label= C2
/note= "Conserved
                                                                                                                                                                                                                              Location/Qualifiers
                                                                             'note=
                                                                                        /label=
                                                                                                                                                            109..120
                                                                                                                                                                     /note= "Variable
                                                                                                                                                                               /label=
                                                                                                                                                                                                 'note=
                                                                                                                                                                                                             /label=
                                                                                                                                                                                                                                                                                                                                                   Protein;
                                      . 229
                                                                                                                               .124
                                                                                                                                                                                                                                                                     meningococcal disease;
                                                                                                                                                                                                                                                                                         surface antigen NhhA polypeptide
                                                                             "Conserved
                                                                                                                                                                                                 "Conserved region
                                                                                                                                                                                ≤.
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                                                                                         C3
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                                                                                                                                                                                                                                                  EG329
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                                                                                                                                                                                                                                                                      meningitis vaccine
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                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                       The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhhA (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively inmunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhAA from N. meningitidis strain EG329 is 1 of 10 NhhA polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New NhhA surface antigen polypeptides and polynucleotides
Neisseria meningitidis, useful in producing vaccines for preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preventing broad spectrum of Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYQU ) UNIV QUEENSLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-2001;
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                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                    present invention.
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            272
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                                                  212
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                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                YLDPVLRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ
                                        TDEGEGIVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
                                                                               VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
                                                                                                            GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
                                                                                                                                 GIGSTLTD----
                                                                                                                                                  NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN
                                                                                                                                                            ----FTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fig 1; 91pp;
           SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
                               TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
                                                                      VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
591
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                                                                                                                                                                                                                                                                                96.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Conserved region 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              c_5
                                                                                                                                                                                                                                                                                 Score 2447.5; DB 2
Pred. No. 2.9e-146;
                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                region
                                                                                                                        ---RAASVKDVLNAGWNIKGVK-----NVDF
                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                          Length 591
                                                                                                                                                                                                             -TLKAGDNLKIKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treating
                                                                                                                                                                                                                                                                        99;
                                                                                                                                                                                                                                                                       Gaps
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RESULT 9
AAU06182
The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhha (AAU06182-AAU06185). The modified or mutant Nhha polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence represents N. meningitidis strain PMC21 surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N. meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU06182 standard;
                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                            New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Surface
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                                                                                                                                                                                                                                                 12; Fig 5; 91pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                 Jennings MP
                                                                                                                                                                                                                                                                                         broad spectrum
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52..512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PMC21 NhhA deletion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NhhA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Mature_NhhA_deletion_mutant_#1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               meningococcal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Predicted mature protein, claimed in claim 12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal_peptide
                                                                                                                                                                                                                                                                                           of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                512
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deletion mutant

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RESULT 10
AAY23743
ID AAY237
XX
AC AAY22
XX
DT 08-SJ
DT 08-SJ
DX A Su
DX A Su
DX A Su
CX Immu
XX
CS Nei:
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CS
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Pred. No. 2.8e-142;
Pred. No. 2.8e-142;
                                                                IRA;
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RESULT 11
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Best Local S
Matches 489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis surface meningitidis infections
                                                                                   AAU06176
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||KIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL
                                                                                   standard;
                                                                                                                                                              AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                                                                                                            KKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQ
                                                                                                                                                                                                                                                                GKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDG-DALNVGS
                                                                                                                                                                                                                                                                                                Page 114-115; 132pp;
                                                                                                                                                AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                                                                                                                                                   GKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDKGALNVGS
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81.6%;
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Pred. No. 1.8e
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No. 1.8e-141;
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N. meningitidis H38

surface antigen

NhhA polypeptide sequence

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Query Match
Best Local Similarity
                                                 The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhhA (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhA from N. meningitidis strain H38 is 1 of 10 NhAA polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                     Claim
                                                                                                                                                                                                    New NhhA surface antigen polypeptides and polynucleotides Neisseria meningitidis, useful in producing vaccines for preventing broad spectrum of Neisseria meningitidis -
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N-PSDB; AAX85792.
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Matches 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also
                                       21-FEB-2000
                                                                                             AAY57044 standard;
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WPI; 2000-053103/04.
N-PSDB; AAZ39864.
                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                New polypeptide from neisseria meningitidis useful for diagnosis, treatment or prevention of bacterial infections in mammal
                                                                                                                                                                                                       Ruelle
                                                                                                                                                                                                                                 13-MAY-1998;
                                                                                                                                                                                                                                              07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                 BASB029; Nisseria meningitidis; surface fibril protein;
                                                                                                                                                                                                                                                                        WO9958683-A2
                                                                                                                                                                                                                                                                                                              Neisseria
                                                                                                                                                                                                                                                                                                                          infection; treatment; prevent; antibacterial drug
                                                                                                                                                                                                                   (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                           18-NOV-1999
                                                                                                                                                                                                                                                                                                              meningitidis
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                                                                                                                                                                                                                                                                                            104
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                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                    "Encoded
                                                                                                                                                                                                                                                                                    by AATC'
                                                                                                                                                                                                                                                                                                                                  HSF;
                                                                                                                                                                                                                                                                                                                                 diagnosis;
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This is the Nisseria meningitidis BASB029 amino acid sequence from CC serogroup B strain ATCC13090. The BASB029 protein is homologous to the CC Haemophilus influenzae surface fibril (HSF) protein. The invention CC relates to BASB029 polynucleotide sequences (AAZ39864-Z39865) and CC polypeptide sequences (AAY57044-Y57045) and their immunogenic fragments. CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria CC meningitidis infection in a mammal. Compositions containing BASB029 CC polynucleotides and polypeptides are useful for generating an immune CC response in an animal. A therapeutic composition comprising an antibody CC directed against BASB029 is useful in treating humans with Neisseria CC meningitidis disease. The polynucleotide is useful in the diagnosis of CC the stage of infection, type of infection, susceptibility to an CC infection which results from increased or decreased expression of the polynucleotide, and for therapeutic or prophylactic purposes, particularly genetic immunisation. Antibodies against BASB029 CC particularly bacterial infections. The protein is useful in the CC creativing the protein suseful for treating infections corrections useful in the protein suseful in the protein suseful for the protein suseful for the protein suseful in the protein suseful in the protein suseful for the protein suseful in the protein suseful s receiving the protein. organism

Claim 4; Fig 2; 74pp; English

Sequence 594

Length

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                                                                    NTNASSFTYSLKKDLTDLTSVGTEKLSFSANSNKVNITSDTKGLNFAKKTAETNGDTTVH
                                                                                                                PVQRTAVVLSFRSDKEGTGEKEVTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE
                                              LNGIGSTLTD---
                        LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV
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nilarity 82.0%;
Conservative
                                                                                -FTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVH
                                                                                                                                                                                                       Score 2366; DB 21;
Pred. No. 4e-141;
4; Mismatches 11;
                                             -RAASVKDVLNAGWNIKGVK-----
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          25-JAN-2001; 2001WO-AU00069
                             02-AUG-2001
                                               WO200155182-A1
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                                                                                                                                                                                                                                                                                                                                                             antigen NhhA; meningococcal disease;
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                                                                                                                                                                                                                                                          /note= "Variable region
105..116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhhA (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New NhhA surface antigen polypeptides and puneisseria meningitidis, useful in producing preventing broad spectrum of Neisseria meni
                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence representing the wild type surface antigen Nhha from N. meningitidis strain EG327 is 1 of 10 Nhha polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
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                                                                                                                                PVQRTAVVLSFRSDKEGTGEKEVTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE 120
                                                                                                                                                                       DFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKDKGEND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fig 1; 91pp;
 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                             TVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE
                                                                                                                                                                                                           LNGIGSTLIDILLNIGATINVINDNYIDDEKKRAASVKDVLNAGWNIKGVKPGITASDNV
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82.0%;
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Pred. No. 4e-1
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                                                                                                                                                                                                                                                                                                                         The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kba. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the Netection or diagnosis of N. meningitidis infection in humans are necessarily as the Netection or diagnosis of N. meningitidis infection in humans.
                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                             The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 95-97; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Surface protein; surface immunoreactive peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A surface protein of Neisseria
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                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis surface proteins useful for treating meningitidis infections
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N-PSDB; AAX85791.
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                                                                 DFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENG
                                               LNGIGSTLTD-----
                                                                                                                PVQRTAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE 120
                      LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV
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Pred. No. 1.1e-140;
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                                                                                                                                                               PVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPG
                                 PVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPG
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Search completed: October 6, 2003, 09:22:36
Job time: 46.1096 secs

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1: /cgn2_6/ptodata/1,
2: //gn2_6/ptodata/1,
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Sequence 21, Appli Sequence 2, Appli Sequence 2, Appli Sequence 11, Appli Sequence 11, Appli Sequence 15, Appli Sequence 19, Appli Sequence 19, Appli Sequence 7, Appli Sequence 13, Appli Sequence 13, Appli Sequence 14, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 19, Appli Sequence 30, Appli Sequence 4, Appli Sequence 2, Appli
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Sequence 28, Appl	Sequence 24, Appl	•	•	Sequence 15, Appl		Sequence 4, Appli	Sequence 4, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 44, Appl	Sequence 32, Appl	Sequence 2, Appli	Sequence 32, Appl

RESULT 1
US-09-377-155-21
Sequence 21, Application US/09377155
Patent No. 6197312
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul

271	VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS 300 TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV 271	241 VRTYDTVE 212 TDEGEGLV	Qу	
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240	GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF 24	181 GIGSTLTD	Db	
151	NASYKDVLNAGWNIKGVKNVDF	121 GIGSTLTD	Qy	
180	_	121 NGTNFTYS	Db	
120	FTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN 12	65FTYS	Qy	
120	YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 12	61 YLDPVQRT	DЬ	
64	~	53	Qy	
60	MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL 60	1 MNKIYRII	Db	
52	1	1 MNKIYRII	Qy	
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		tch	Query Match	
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		: 591	. TYDE: DET	
			; SEQ ID NO 21	
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	1997-12-12	PRIOR FILING DATE: 1997-12-12	; PRIOR F	
	APPLICATION NUMBER: GB 9726398.2	PPLICATION N		-
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	1999-08-19 MRER: PCT/AII98/01031	PPLICATION N	· PRIOR A	
	CURRENT APPLICATION NUMBER: US/09/377,155	APPLICATION	; CURRENT	
	064/0128	FILE REFERENCE: 065064/0128	; FILE RE	
	/ENTION: NOVEL SURFACE ANTIGEN	¥ ::	TITLE OF I	
	JENNINGS, Michael Paul		; APPLICANT:	

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Sequence 21. Application US/0966974

Patent NO. 6333173

GENERAL INFORMATION:

APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: DENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard

TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128

CURRENT APPLICATION NUMBER: US/09/669,974

CURRENT FILING DATE: 1909-08-19

PRIOR APPLICATION NUMBER: US/09/377,155

PRIOR APPLICATION NUMBER: PCT/AU98/01031

PRIOR FILING DATE: 1998-12-14

PRIOR FILING DATE: 1998-12-14
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TDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
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                                                              VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
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CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
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Best Local Similarity
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APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE AN
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                                                                             STDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTAT
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VSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDET
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CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
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                                                         VSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDET
                                                                                                                STDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKEETVTSGTNVTEASGKGTTAT
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Pred. No. 3.4e-187;
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PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 11
SEQ ID NO 11
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CURRENT FILING DATE: 1999-08-19
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                                                                                                 SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
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CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
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PRIOR ETLING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
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CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
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                                                                                                                                                              --- NVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLYTGKD
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             AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                  KGENGSSTDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETYTSGTNYTFASG
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                                                                                                                                                                                                                                                                                                                                                               DTTVHLNGIGSTLTD--------
                                                                                                                                                                                                                                                                                                                                                                                            KNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNG
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AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                                                                                                                       KGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASG
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nilarity 81.6%;
Conservative
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065064/0128
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pred. No. 1.5e-180;
2; Mismatches 11;
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CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-13-12
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Best Local
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APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
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                                                                                                                     GKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDG-DALNVGS
                                                                                                                                                                                 KGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSK 324
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                AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                            KKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQ
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AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                            KDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQ
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Pred. No. 1.5e-180;
Pred. No. 1.5e-181;
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RESULT

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RESULT 10 US-09-669-974-9 ; Sequence 9, Application ; Patent No. 6333173

US/09669974

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GENERAL INFORMATION:

360 264 204

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TITLE OF INVENTION: NOVEL SURFACE ANTIGEN FILE REFERENCE: 06504/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 199-08-19
PRIOR APPLICATION NUMBER: CT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
PRIOR PRIOR FOR DID NOS: 3
SOFTWARE: PatentIn Ver: 2.0
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Best Local S
Matches 487
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APPLICANT: PEAK, Ian Richard
APPLICANT: JENNINGS, Michael
APPLICANT: MOXON, E. Richael
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TYPE: PRT

ORGANISM: Neisseria meningitidis
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                                                                       PVRITNVAPGVKEGDVTNVAQLKGVAQNLNNHIDNVDGNARAGIAQAIATAGLVQAYLPG
                                                                                          PVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPG
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Pred. No. 4.1e-180;
4; Mismatches 11;
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US-09-377-155-7
US-09-377-155-7
; Sequence 7, Application U
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Ri
; APPLICANT: JENNINGS, Mi
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APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
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US-09-669-974-9
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TYPE: PF
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Mismatches
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No. 4.1e-180;
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PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 594
TYPE: PRT
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US-09-377-155-7
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Best Local S
Matches 487
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CURRENT FILING DATE: 1999-08-19
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TITLE OF INVENTION:
FILE REFERENCE: 065
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                                                        PVRITNVAPGYKEGDYTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPG
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Pred. No. 1.5e-179;
2; Mismatches 13;
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Sequence 7, Application US/09669974

Patent No. 633173

GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065664/0128

CURRENT APPLICATION NUMBER: US/09/669,974

US-09-669-974-7

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RESULT 13
US-09-377-155-13
US-09-377-155-13
; Sequence 13, Application U
; Patent No. 6197312
; GENERAL INFORMATION:
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US-09-669-974-7
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PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
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Best Local
  APPLICANT: PEAK, Ian Richard Anselm APPLICANT: JENNINGS, Michael Paul APPLICANT: MOXON, E. Richard TITLE OF INVENTION: NOVEL SURFACE ANTIGEN FILE REFERENCE: 065064/0128 CURRENT APPLICATION NUMBER: US/09/377,155 CURRENT FILING DATE: 1999-08-19 PRIOR APPLICATION NUMBER: PCT/AU98/01031
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                                                SURFACE ANTIGEN
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Pred. No. 1.5e-179;
2; Mismatches 13;
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: MCNON, E. Richard
TITLE OF INVENTION: NOVEL SURPACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
                                                                                                                                             US-09-669-974-13; Sequence 13, Appli; Patent No. 6333173
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US/09669974

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; ORGANISM: Neisseria
US-09-377-155-13
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SOFTWARE: PatentIn V
SEQ ID NO 13
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YLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 502
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Pred. No. 2.3e-178;
3; Mismatches 15;
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Sequence 5, Application US/09377155

Patent No. 6197312;
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: DENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 055064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR APPLICATION NUMBER: GB 9726398.2
VINMEER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
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US-09-669-974-13
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NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 598
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Best Local Similarity
Matches 484; Conserv
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Search completed: October 6, 2003, 09:35:51
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hypothetical prote
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Rappuoli, R.; strain MC58.

Eisen,

180 120

120 64 60

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240 151

211

271 300

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C; Geneti
A; Gene:
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A;Title: Complete DNA sequence of a serogroup A strain of A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: A81888
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A; Residues: 1-592 < PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: GB:AL162755;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                        483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKS
                          NINAGNNIEISRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPV
                                      NINAGNNIEITENGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSKKDNKPV
                                                                                                                                                                                                                             GIGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNIKGVKTGSTTGQSENVDF
                                                                                                                                                                                                                                                       GIGSTLTD-----
                                                                                                                                                                                                                                                                                NASSFTYSLKKDLTGLINVETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN
                                                                                                                                                                                                                                                                                                                                 ESVQRSVVGSIQASMEGSGELETISLSMTNDSKEFVDPYIVVTLKAGDNLKIKQNTNENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NINAGNNIEITRNGKNIDIATSMTPQFSSYSLGAGADAPTLSVDGDALNYGSKKDNKPVR
                                                                                                                                                                                                                                                                                                       ----FTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M.; James,
.; Leather,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GB:AL157959; NID:g7379742; A, strain Z2491
                                                                                                                                                                                                                                                                                                                                                                                                                                     6;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2351; DB 2;
Pred. No. 3.6e-118;
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S.; M
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .; Bentley,
Moule, S.;
                                                                                                                                                                                                                                                       --RAASYKDYLNAGWNIKGVK-----NVDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mungall,
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Rajandream
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R; Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weldman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A; Reference number: A64000; MUID:95350630; PMID:7542800
A; Accession: I64138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adhesin homolog HI1732 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Oct-1997
C;Accession: I64138
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A; Residues: 1-298 <T:
A; Cross-references: (
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  238
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                                                                                                                                                                                                                                                                                                                                                       1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQA----
                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
VSDTLTIGGNTPAAGGATPKVSITSTADGLKLAK---GTNGDTAVHLNGLASTLPDVTTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                   TGASTSVTFSPSDIEKTRAATIKDVLNAGWNIKGAKVAGGNTENVDLVAGYDNVEFITGD
                                                                                                                                                                                                           GTEKLSFSAN---
                                                                                                                                                                                                                                                  STEDDIEDSAATKODNKNQALKAGDTLTLKAGKNLKAKLDQGGKSVTFALAKDLDVKTAK 120
                                                                                                                                                                                                                                                                                                                                  MNKIFKVIWNVVTQTWVVVSELTRAHTKRTSATVATAVLATVLSATVQAINDAGTFVKVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKS
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                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <TIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB:U32846; GB:L42023; NID:g1574588; PID:g1574589; TIGR:HI1732
                                                                                                                                                                                                                                                                                                                                                                                                                                    20.6%;
                                                                                                                          -RAASVKDVLNAGWNIKGVK-----NVDFVRTYDTVEFLSAD
                                                                                                                                                                                                         -GNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTD----
                                                                                                                                                                                                                                                                                           -----KQFTYSLKKDLTDLTSV
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 523.5; DB Pred. No. 4.2e-21
                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                            298;
                                                                                                                                                                                                                                                                                                                                                                                                                   81;
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surface protein XF1981 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa (c;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000 C;Accession: A82615 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucle Nature 406, 151-157, 2000 for Nucleotide

A;Title: The genome sequence of the plant pathogen Xylella A;Reference number: A82515; MUID:2035717; PMID:10910347 A;Note: for a complete list of authors see reference number A;Accession: A82615 A59328

Status: preliminary

A;Molecule type: DNA A;Residues: 1-1190 <SIM> A;Cross-references: GB:AE004017; GB:AE003849; NID:g9107083; PIDN:AAF84783.1; GSPDB:GN

A;Experimental source: strain 9a5c R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargas-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.F submitted to GenBank, June 2000 A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S. Camargo, Ini, A.P.; F.A.; Acencio, L.E.A.; Carraro, Ferreira, A.J.S. M.; Alvarenga, R.
raro, D.M.; Carrer

J.S.; Franca, တ . . Franco, FΥ

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R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: A86036
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1588 <570>
A;Cross-references: GB:AE005174; NID:g12518349; PIDN:AAG58749.1;
                                                                                                                                                                                                                                                                                                                     RESULT
A86036
                                                                                                                                                                                                                        probable adhesin Z5029 [imported] - Escherichia col
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001
C;Accession: A86036
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                              VFKFSGSANTRSQVGIGAGVGYQW 1190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVITDGPSVTSSGINAGSQKITNVAAGTADTDAVNLSQLNTAMAGSGAKSVHYYSTYD--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVVSELTRNHTKRASATVKTAVLATLLFATVQASANTLKAGDNLKIKQFTYS--LKKDLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVVGSLRRDTDGGVAAAIATANLPQAYIPGRGMTSVGVSSYRGQSAIAVGVSSVSESGRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADNAVAIGHHSVADRANTVSVGSAGSERQVTNVAAGTADTDAVNVSQLNQGLITAKQYTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSV----DGDALNVGSK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STLTDRAASVKDVLNAG----WNI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLKNTDGNIVISKESGSNDVLFNLSS---SLKLDKLTVGDTVMTTNGVTVGSGVTLGSMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NSLNN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NITVMYDVNVGDALNVNQL----QNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNI 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVASADGSVALGD-GAKDGARGAESYTGKYSGLQNNTVGTVSVGDASKGETRTVS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENG-SSTDEGEG
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Pred. No. 9.9e-13;
72; Mismatches 211;
                                                                                                                                                                                                                                                                                            Escherichia coli (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -RITNVAPGVKEGDVTNVAQLKGVAQNLNNRID
      PIDN:AAG58749.1; GSPDB:GN00145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----KGVKNVDFVRTYDTV 158
                                                                                                                                                                                                                                                  #text_change 14-Sep-2001
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                                                                                                                                       0157:H7
                                                                                                                                                                                J.D.; Rose, Potamousis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              478
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                                                                                                                                                                              D.J.; Mayhev
K.; Apodaca,
      UWGP: 250
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A;Molecule type: DNA
A;Residues: 1-1588 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB37903.1; PID:gl3363955;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs4480
                                                                                                                                                                                                                                                                               gasawara, N.; Yasunaga, T
DNA Res. 8, 11-22, 2001
A;Title: Complete genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Experimental source: strain O157:H7, substrain C;Genetics: A;Gene: Z5029
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A; Accession: H91188
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gasawara, N.; Yasunaga, T.; Kuhara, S.;
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Best Local
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                                                    Local 141;
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                                                                                Similarity
TVRQLQNAIGAVATTPTKYFHANSTEE--DSLAVGTDSLAMGAKTIVNGDKGIGIGYGAY 1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNIENGIGDIVTTGSTKYFKTNTDGVDA--SAQGKDSVAIGSGSIAAAD--NSVALGTG- 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDTKGLNFAKETAGTNGDTTVHLNGI----GSTLTDRAASVKDVLN--AGWNIKG---VK 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TVRQLQNAIGAVATTPTKYFHANSTEE -- DSLAVGTDSLAMGAKTIVNGDKGIGIGYGAY 1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TVQASANTLKAGDNLKIKQFTYSLKKDLTDLTSVGTEKLSFSA----NGNK-----VNIT
                               TVQASANTLKAGDNLKIKQFTYSLKKDLTDLTSVGTEKLSFSA----NGNK-----VNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STNSQGEYSAALGAGIQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---ENG----SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SADGQRQITNVAAGSADTDAVNVG-----QLKVTDAQVSQNTQSITNLDNR-VTNLDSRV 1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKG- 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VDANALNGI--AIGSNAQ-VIHVNSIAIGNGSTTTRGAQTNYTAYNMDAPQNSVGEFSVG 1285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGNSRGHFGASASVGYQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TFASGKGTTATVSKDDQGNIT-VMYDVNVGDALNVNQLQNS---GWNLDSKAVAGSSGKV 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD
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                                                                                                                                                                                                                                                                     sequence of enterohemorrhagic Escherichia 29; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----RISNVSAGVNNNDVVNYAQLKQSVQETKQYTDQRMVEMDNKLSKT
                                                                                14.2%;
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Pred. No. 1.7e-11;
                                                                Score 360.5; DB 2;
Pred. No. 1.7e-11;
5; Mismatches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 181;
                                                                                                                                                                                                                                                                                                                    Kurokawa, K.; Ishii, K.; Yokoyama, Shiba, T.; Hattori, M.; Shinagawa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----YSNITLGGGNGGTT----
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                                                                                              Length 1588
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                                                                                                                                                                                  GSPDB:GN00154
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                                                                Gaps
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                                                                  21;
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1536

VVVNDLGLSIVGGASLTLSGINAGSHKITNVTAGTEDTDAVNFSQLKSVSEAVDKGWT-L 1594

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A;Ittle: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Rote: for a complete list of authors see reference number A59328 below
A;Accession: D82671
A;Status: preliminary
A;Molecule type: DNA
A;References: GB:AE003982; GB:AE003849; NID:g9106554; PIDN:AAF84338.1; GSPDB:GN001
A;Accession: 1-2059 <SIM>A;Residues: 1-2059 <SIM>A;Residues: 1-2059 <A;Reinach, F.C.; Arruda, P.; Abreu, F.A.; Accencio, M.; Alvarenga, R.; A
B;Cross-references: GB:AE003982; GB:AE003849; NID:g9106554; PIDN:AAF84338.1; GSPDB:GN001
A;Experimental source: strain 9a5c
R;Simpson, A.J.G; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Carraro, D.M.; Carrer, H.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Franca, J.S.; Franca, S.C.; Franco, M.C.; Frohn
J.D.; Junqueira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohn
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marrino, C.L.; Marrins, E.
B.; Authors: Astins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.R.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santellil, R.V.; Sawasak
A; Authors: da Silva, A.C.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, F.R.; da Silvai, A.M.; Silvaid.
B.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.E.;
A; Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    surface protein XF1529 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-A C;Accession: D82671 R;anonymous, The Xylella fastidiosa Consortium of the Organization f Nature 406, 151-157, 2000
  Qγ
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                                                                              Query Match
Best Local Similarity
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VVVSELTRNHTKRASATVKTAVLATLLFATVQASANTLKAGDNLKIKQFTYSLKKDLTDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTA 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQ------NLNNRIDNV 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVATEENTISVGSSTNQRRITNVAAAGKNATDAVNVAQLKSSEAGGVRYDTKA------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VDANALNGI--AIGSNAQ-VIHVNSIAIGNGSTTTRGAQTNYTAYNMDAPQNSVGEFSVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDTKGLNFAKETAGTNGDTTVHLNGI----GSTLTDRAASVKDVLN--AGWNIKG---VK
                                                      Conservative
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                                                                              14.1%;
25.3%;
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                                                      85;
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                                                 Score 358.5; DB 2;
Pred. No. 2.9e-11;
5; Mismatches 202;
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                                                 Indels 144;
                                                                                                   Length
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                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AL513382;
C;Genetics:
A;Gene: sapB
                                                                                                                                                                                                                                                                                                                                                                          th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dow
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AC0976
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1107 <PARP
                                              Q
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                                                                                LLWDEDTGAF-
                                                                                                                                                                                                                             Similarity.
     SAIADINTSITNLGTDALSW----
                                                    YSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKE-TAGTNGDTTVHLNGIGST
                                                                                                                                                    IIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANTLKAGDNLKIKQFT
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                                                                                                                                                                                                        Conservative
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21
                                                                                                        ---SANHGGSTSKITNVAAGALSEDSTDAVNGSQLYE-TNQKVDQNT
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30 de
7:
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Pred.
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                                                                                                                                                                                                                             351.5;
No. 3.2
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Salmonella
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, L.; White, N.; Farr
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RESULT 9 AH0110 Probable surface C; Species: Yersi C; Date: 02-Nov-2 C; Accession: AH0 R; Parkhill, J.; deno-Tarraga, A.; il, M.; Rutherfo Nature 413, 523- A; Title: Genome A; Reference numb A; Accession: AH0 A; Status: prelim A; Molecule type: A; Cross-referenc C; Genetics: A; Gene: YP00902 Query Match Best Local Sim Matches 134; Qy 12 AL Db 213 AL	0y 0y 0y 0y	Qy Qy Db	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
AHO110  AHO110  Probable surface protein (partial) YPO0902 [imported] - Yersinia pestis (strain CO92) C; Species: Yersinia pestis  C; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001  C; Accession: AH0110  R; Parkhill, J; Wreen, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-537, 2001  A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.  A; Reference number: AB0001; MUID:21470413; PMID:11586360  A; Recession: AH0110  A; Status: preliminary  A; Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:g15978974; GSPDB:GN00175  A; Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:g15978974; GSPDB:GN00175  C; Genetics: A; Gene: YPO0902  Query Match Best Local Similarity 25.3%; Pred. No. 3.1e-11; Matches 134; Conservative 76; Mismatches 198; Indels 121; Gaps 21; Matches 134; Conservative 76; Mismatches 198; Indels 121; Gaps 21;  Dy 12 ALNAWYVSELTRNHTKRASATVKTAVLATLLFATVQASANVTLKAGDNLKIKQFTY 67	412	315 VISGNVSPSKGKMDETVNINAGNNIEITRNGKNI	126 LTDRAASVKDVLNAGWNIKGVKNVDFVRTYDTVEFLSADTKTTTVNVE 173
A; Reference A; Accession A; Status: r A; Status: r A; Status: r A; Cross-rei A; Cross-rei A; Cross-rei Biochim. Bi Biochim. Bi Biochim. Bi Biochim. Bi A; Title: Ar A; Reference A; Accessior A; Status: t A; Molecule A; Residues: A; Cross-rei A; Cross-rei A; Cross-rei C; Genetics: A; Cross-rei C; Genetics: A; Cross-rei C; Function: A; Descriptics: C; Keywords: C; Keyw	RESULT 10 A64905 ydeK protein N;Alternate r C;Species: Es C;Date: 12-Se C;Accession: R;Blattner, I A; Rose, D Science 277, A;Title: The	Qy Db Db	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
	4905 4905 4905 48 Protein - Escherichia coli (strain K-12) Alternate names: protein T Species: Escherichia coli Date: 12-Sep-1997 **sequence_revision 17-Sep-1997 **text_change 01-Mar-2002 Accession: A64905; I52440; S34315 Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; i.; Rose, D.J.; Mau, B.; Shao, Y. i.ence 277, 1453-1462, 1997 Title: The complete genome sequence of Escherichia coli K-12.	355 TPQFSSYSLGAGADAPTLSVDGDALNYGSKKDNKPVRITNVAPGVKEGDV 404 :  :   :         :   :   :         :	68 SLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIG 123

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surface-exposed outer membrane protein XF1516 [imported] - Xylella fastidiosa (strain 9a Ci9acies: Xylella fastidiosa (strain 9a Cipate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C;Accession: C82672 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen A;Titte: The genome sequence of the plant pathogen Xylella fastidiosa. A,Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 below A;Accession: C82672 A;Status: preliminary A;Accession: C82672 A;Status: preliminary A;Molecule type: DNA A;Cross-references: GB:AE003981; GB:AE003849; NID:99106543; PIDN:AAF84325.1; GSPDB:GN001 A;Experimental source: strain 9a5c R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Accencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H Briones, M.R.S.; Bueno, M.R.P.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr chado, M.A.; Madeira, A.M.B. N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menok, C.F.M.; Miracca, E.C.; Migaki, C.Y.; F.G.; Migaki, C.Y.; Sosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santellii, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvei, M.S.; Mar, M.A.; da Silvei, A.M.; Silva Jr., W.A.; da Silvei, A.M.; Silva Jr., W.A.; da Silvei, M.A.; da Silvei, M
A;Contents: annotation C;Genetics: A;Gene: XF1516
                                                                        M.; Tsuhako, M.H.; Vallada
A;Reference number: A59328
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A;Gene: hmwA
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A;Title: Genome sequence of Yersinia pestis, A;Reference number: AB0001; MUID:21470413; PM A;Accession: AF0394
A;Status: preliminary A;Molecule type: DNA A;Residues: 1-1910 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                   probable adhesin hmwA [imported] -
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revis
C;Accession: AF0394
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A;Cross-references: EMBL:X65022; NID:g42254; PIDN:CAA46156.1; R;Benz, I.; Schmidt, M.A. Mol. Microbiol. 6, 1539-1546, 1992 A;Title: AIDA-I, the adhesin involved in diffuse adherence of A;Reference number: S22680; MUID:92326638; PMID:1625582 A;Accession: S22680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adhesin AIDA-I precursor - Escherichia coli plasmid pIB6
C;Species: Escherichia coli
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 08-Oct-1999
C;Accession: S28634; S22680; S28881; S72657
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S28634
A; Molecule type: pro
A; Residues: 847-856
A; Experimental source
                                                 A; Experimental source: strain 2787
R; Suhr, M.; Benz, I.; Schmidt, M.A.
Mol. Microbiol. 22, 31-42, 193.
A; Title: Processing of the AIDA-I precursor: removal of A; Reference number: $72657; MUID:97055419; PMID:8899706
A; Accession: $72657
                                                                                                                                                        A; Molecule type: protein A; Residues: 50-56 <BE3>
                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 839-1286 <BE2>
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A; Residues: 1-1286 <BEN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTVSSGET----QIVYSGRGNSNATVNSGGTQIVN---NGGKTTATTVNSS----GSQNVG
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                         AQAIATAGLVQAYL---PGKSMMAIG----
                                                                                                                                                                 YARGTILNNSGRENVSNGGVSYNAMINTGGNQYIYSDGEATAAIVNTSGFQRIN--SGGT
                                                                                                                                                                                                                        SEGTAINTLYSDGGYQHIRNGGIASGTIVNQSGYVNISSGGYAESTIINSGGTLRYLSDG
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LQAVSSGGKASATVINEGGAQFVYDGGQVTGTNIKNGGTIRVDSGASALNIALSSGGN
                                                     NLSGRLNAFAGNVVGTILNQEGRQYVYSGATATSTVGNNEGREYVLSGGITDGTVLNSGG
                                                                               NVA-QLKGVAQNLNNRIDNVDGN--
                                                                                                            APVQNSVVVTRTVSSAAKPFDAEVYSGGKQTVYLWRGIWYSNFLTAVWSMFPGTASGANV 511
                                                                                                                                       AP-----TLS-----VDGDALNVGSKK----
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                        -GGTYRGEAGYAIGYSSISDGGN
                                                                                                                                      -----DNKPVRITNVAPGVKEGDVT
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RESULT 14 E90893

A; Declaration Fig. DNA A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-1343 <HAY>
A; Residues: 1-1343 <HAY>
A; Cross-references: GB:BA000007; PIDN:BAB35540.1; PID:g13361583; GSPDB:GN00154
A; Cross-references: GB:BA000007; PIDN:BAB35540.1; PID:g13361583; GSPDB:GN00154 gasawara, N.; Yasunaga, T.; Numaru, J., Elemente et al. 11-22, 2001
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Es hypothetical protein ECs2117 [imported] - Escherichia coli (strain C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 18-C;Accession: E90893 C;Accession, L., C R;Hayashi, T.; Makino, K.; C N: Yasunaga, T.; A; Reference number: A99629; A; Accession: E90893 A; Status: preliminary Ohnishi, M.; ; Kuhara, S.; Kurokawa, K.; Shiba, T.; Hai Hattori, Ishii, K.; Escherichia : : Shinagawa, 18-Jul-2001 Yokoyama, coli 0157:H7 O157:H7, Ξ × substrain Han,

•	32;	Score 208; DB 2; Length 1091;   Score 208; DB 2; Length 1091;   Pred. No. 0.0014;   Fred. No. 197; Indels 168; Gaps   VSELTRNHTKRASATVKTAVLATILFATVQA
	Riley, M.; Cd	ein b2000 - Escherichia coli (strain K-12) ichia coli 10
		Qy 448GKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSR 489   ::
Search completed: October 6, 2003, 09:33:25 Job time: 17.3699 secs	447 503	Qy 388 KPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLP 4
Qy 468 GYSSISDGGNWIIKGTASGN 487   :::::  :         Db 502 GTTTLNNGAILTLSGKTVNN 521	387	Qy 341 ITRNGKNIDIATSWTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDN 3
Qy 408 AQLKGVAQNLNNRIDNVDGNARAGIAQAIATA    :	340	Qy 287 VGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIE 3
Qy 348 IDIATSMTPQFSSVSLGAGADAPTLSVDGDAL  :   :	286	Qy 248 DKFETVTSGTNVTFASGKGTTATVSKDDQCNITVMYDVN 2
Qy 288 GDALNVNQLQNSGWNLDSKAVAGSSGKVISGN	247 .	Qy 197 GK-LVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGOTGQA 2
Qy 236KTTTANGQTGQADKFETVTSGTNVTFASG	196	Qy 169TVNVESKDNGKKTEV-KIG
Qy 188 KTSVIKEKDGKLVTGKDKGENGSSTDEG	168 170	Qy 111 TNGDTTVHLNGIGSTLTDRAASVKDVLNAGWNIKGVKNVDFVRTYDTVEFLSADTKTT 1
Qy 142 NI	112	
Qy 101 GLNFAKETAGTNGDTTVHLNGIGSTLTDRAAS		Qy 1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQAS 50
Qy 51 ANTLKAGDNLKIKQFTYSLKKDLTDLT	27;	Query Match 8.2%; Score 208.5; DB 2; Length 1343; Best Local Similarity 23.6%; Pred. No. 0.0017; Matches 140; Conservative 72; Mismatches 239; Indels 141; Gaps
Db 57 LNTCYRLVWNHMTGAFVVASELARARGKRGGV		A;Gene: ECs2117

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	502 GTTTLNNGAILTLSGKTVNN 521	da da	145
	468 GYSSISDGGNWIIKGTASGN 487	Qy	187
GTLA 501	468 MLEKGSSFTLNAGDTATDTTVNGGLFTARGGTLA 501	Дb	192
GYAI 467	408 AQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAI 467	Qy	340
ADAL 467	426GTATTVSMGNGGVLLADSGAAVSGTRSDGKAFSIGGGQADAL 467	Db	841
VTNV 407	348' IDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNV 407	Qy	286
NG 425	388 GKADNV-VLENGG-RLDVLTGHTATNTRVDDGGTLDV-RNG 425	ф	284
NGKN 347	288 GDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKN 347	Qy	247
SVVE 387	334 GVAGNTTVN-QKGRL-QVDAGGTATNVTLKQGGALVTSTAATVTGINRLGAFSVVE 387	Db	230
DVNV 287	236KTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQG-NITVMYDVNV 287	Qγ	196
VKNG 333	283 NTTVVYAGGDQTVHGHALDTTLNGGYQYVHNGGTASDTVVNSDGWQIVKNG 333	Db	L70
1 235	188 KTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRM	Qy	89
EGTA 282	227 QVVKPGTVATDTVVNTGAEGGPDAENGDTGQFVRGDAVRTTINKNGRQIVRAEGTA	Дb	112
(IG-A 187	142 NIKGVKNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIG-A 187	Qy	110
IDKGW 226	171 GLQ-RVNPGGSVSDTVISAGG-GQSLQGRAVNTTLNGGEQWMHEGAIATGTVINDKGW 226	Db	50
GW 141	101 GLNFAKETAGTNGDTTVHLNGIGSTLTDRAASVKDVLNAGW 141	Qy	50
SG 170	117 GGTLANHDNQIVFGTTNGMTISTGLEYGPDNEANTGGQWVQDGGTANKTTVTSG 170	Db	27;
SDTK 100	51 ANTLKAGDNLKIKQFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTK 100	Qy	
ETVN 116	57 LNTCYRLVWNHMTGAFVVASELARARGKRGGVAVALSLAAVTSLPVLAADIVVHPGETVN 116	dd da	

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Result
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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     MNKIYRIIWNSALNAWVVVS.....TASGNSRGHFGASASVGYQW
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45	44	43	42	41	40	39	38	37	36	35	34
147.5	148	148.5	149	149.5	150	150	150	150.5	150.5	151	151
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Q9zlt1 helicobacte		Q8x8v7 escherichia	052959 salmonella								033479 pseudomonas

## ALIGNMENTS

666666666666666666666666666666666666666	RESULT  YDEK_E  YDEK_E  ID EK_E  DT 0  DT 1  DE H  GN E  OC B
SEQUENCE FROM N.A.  STRAIN-K12 / MG1655;  MEDLIKE=97426617; pubMed=9278503;  Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  Gregor J., Davis N. M., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  Mu B., Shao Y.;  "The complete genome sequence of Escherichia coli K-12.";  Science 277:1453-1474(1997).  SQUENCE FROM N.A.  STRAIN-K12;  MEDLIKE=97251357; PubMed=9097039;  Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,  Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,  Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,  Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,  Kasai H., Kashimoto K., Sivasundaram S., Tagami H., Takeda J.,  Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;  "A 570-kb Dan sequence of the Escherichia coli K-12 genome  corresponding to the 28 0-40.1 min region on the linkage map.";  DNA Res. 3:363-377(1996).  SEQUENCE OF 595-1325 FROM N.A.  MEDLIKE-94100243; PubMed=8274505;  Cartwright P.J., Timms M.W., Lithgow T., Hoej P.B., Hoogenraed N.J.;  "An Escherichia coli gene showing a potential ancestral relationship  to the genes for the mitochondrial import site proteins ISP42 and  MOM38 ".  BIOCHIM. Biophys. Acta 1153:345-347(1993).  -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor  (Fotential).  -1- SIMILARTY: TO E.COLI YFAL.  -1- SIMILARTY: TO E.COLI YFAL.  -1- SIMILARTY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS  ISP42 AND MOM38  -1- CAUTION: REF. 3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A  FRAMESHICT IN POSITION 653.	YDEK ORDER BISTON STANDARD; PRT; 1325 AA. P32051; P76140; P77168; 01-CCT-1993 (Rel. 27, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 16-CCT-2001 (Rel. 40, Last annotation update) Hypothetical lipoprotein ydek precursor (ORFT). YDEK OR ORET OR BIS10. Escherichia coli. Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Escherichia. NCBI_TaxID=562;

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RESULT
AIDA_EC
ID AI
AC QO
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Best Local S
Matches 146
AIDA_ECOLI STAN
Q03155;
01-JUN-1994 (Rel. 2
01-JUN-1994 (Rel. 2
28-FEB-2003 (Rel. 4
Adhesin aidA-I prec
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EMBL; D90793; BAA15190.1; ALT_INIT.
EMBL; D90794; BAA15197.1; ALT_INIT.
EMBL; X73295; CAA51730.1; ALT_FRAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PS00013; PROKAR_LIPOPROTEIN;
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                                                                                                                                           SGIVNVSNGATLNSTGYGFIGGNASGKGIVNISTDSLWNLK-TSSTNAQ
                                                                                                                                                                      KSMMAIGGGTYRGEAGYAI-----
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                                                                                                                                                                                                                                                                                                               HWNFLGTGEAFRYIYIGDAGDGELNVSSEGKVDSGIITAG - - - MKETGTGNITVKDKNSV
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                                                                                                                                                                                                                          RITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLP-
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  precursor
                                                                       STANDARD;
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1325 HYPOTHETICAL LIPOPROTEIN YDEK.
19 N-ACYL DIGLYCERIDE (POTENTIAL).
184 N -> K (IN REF. 3).
1317 M -> S (IN REF. 3).
AA; 136514 MW; 26A3A066FA19AD7D CRC64;
             . 29, Created)
. 29, Last sequ.
. 41, Last anno
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              Last sequence update)
Last annotation update)
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Pred. No. 0.00018;
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-!- FUNCTION: THIS IS AN ADHESION PROTEIN NECESSARV ADHERENCE OF DIARRHEA-CAUSING ENTEROPATHOGENIC
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PIR; S28634; S28634
InterPro; IPR006315; Autotransport.
InterPro; IPR005546; Autotransporter.
InterPro; IPR004899; Pertactin.
Pfam; PF03797; Autotransporter; 1.
Pfam; PF03212; Pertactin; 1.
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STRAIN=0126:H27 / 2
MEDLINE=92326638; P
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Escherichia
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  334
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                                                                                                                                                                                                                                                                                                                                       TNG---DTTVHLNGIGSTLTDRAASVKDVLNAGWNIKGVKNVDFVRTYDTVEFLSADTK-
                                                                                                                                                                                                                                                                                   GTVSSGET ----QIVYSGRGNSNATVNSGGTQIVN --- NGGKTTATTVNSS ---- GSQNVG
                                                                                                                                                                                                                                                                                                             NTLKAGDNLKIKQFTYSLK-KDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAG
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                             S-GWNLDSKAVAG-----
                                                                                    TNVTFASGKGTTATVSKD--
                                                                                                                                         SSTDEGEGLYTAKEVIDAVNKAGWRMKT-----TTANGQT-----GQADKFETVTSG
    SEGTAINTLYSDGGYQHIRNGGIASGTIVNQSGYVNISSGGYAESTIINSGGTLRVLSDG
                                                       VQTVFAGATVTDTTVNSGGNQNISSGGIVSETTVNVSGTQNIYSGGSALSANIKGSQIVN
                                                                                                                                                                     FSGGITDSTNISSGGQQRVSSGGVASNTTINSSGAQNILSEEGAISTHISSGGNQYISAG
                                                                                                                                                                                                                            TSGATISTIVNSGGIQRVSSGGVASATNLSGGAQNIYNLGHAS----NTVIFSGGNQTI
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21.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                           Score 210;
Pred. No. 0.
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                                                                                 -DQGNITVMYDVNV
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                             SSGKVI--SGNVSPSKGKMDETVNINAGNNIEITRNG
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.0012;
                                                                                                                                                                                                                                                                                                                                                                                              226;
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AG43_ECOLI STANDARD; PRT; 1037 FM.
AG43_ECOLI STANDARD; P97241; Q46771;
P39180; P75614; P76360; P97241; Q46771;
01-FEB-1995 (Rel. 31, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-ML 308-225;
Henderson I.R., Owen I
Submitted (JAN-1997)
                                                                                                                                                                                                                                                                                                                 MEDLINE-97251358: PubMed-9097040;
Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Mizobuchi K., Mori H., Mori T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
STRAIN=K12 / EMG2;
MEDLINE=97443975; PubMed=9298646;
Link A.J., Robison K., Church G.M
                                                                                                                                                                                                                                                                             Yamamoto Y., Horiuchi T.;
"A 460-kb DNA sequence of the Esche corresponding to the 40.1-50.0 min
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STRAIN=K12 / MG16
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                            SEQUENCE OF 53-63.
STRAIN=K12 / EMG2;
                                                                                    43, a unique
Escherichia (
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                                                         e protein complex associated with coll.";
1. 171:3634-3640(1989).
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    Church G.M.;
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EcoGene; EG12686; flu
InterPro; IPR006315;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97257509; PubMed-9103983;
Henderson I.R., Meehan M., Owen P.;
"Antlgen 43, a phase-variable bipartite outer membrane protein,
determines colony morphology and autoaggregation in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Comparing the predicted and observed properties in the genome of Escherichia coli K-12."; Electrophoresis 18:1259-1313(1997).
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InterPro; IPR004899; Pertactin.
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FUNCTION: CONTROLS COLONY FORM VARIATION AND AUT FUNCTION AS AN ADHESIN.
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101-FEB-1994 (Rel. 28, Created)

r 16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

Hypothetical protein ydba.

Escherichia coll.

Bacteria need
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SEQUENCE FROM N.A.
STRAIN=K12 / Mc1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Blattner F.R., Plunkett G. F., Glasner J.D., Rode C.K., Mayhew G.F. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Riley M., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
MEDLINE=97251357; PubMed=9097039;
Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
Kasai H., Mashimoto K., Mori H., Mori T., Motomura
Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura
Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., S
Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,
                                                                                                                                              Science
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ECOGene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN-K1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi "A 570-kb DNA sequence of the Escherichia coli K-12 geno corresponding to the 28.0-40.1 min region on the linkage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical CONFLICT
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L; AE000237; AAC74487.1; ALT_SEQ.
L; D90778; BAA15009.1; ALT_SEQ.
L; D90778; BAA18881.1; ALT_SEQ.
L; D90779; BAA18881.1; ALT_SEQ.
L; X62680; ; NOT_ANNOTATED_CDS.
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                                                                                                          AGNNIETTRNGKNIDIATSMT----PQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR
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P15320;
01-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Bacteriol. 170:3177-3188(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular characterization of the marcescens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-88257037; PubMed-3290200; Poole K., Schiebel E., Braun V.;
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01-NOV-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hemolysin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hemolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Outer membrane. SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ERYTHROCYTES BY INTERACTION REQUIRES SHLB FUNCTION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     requires a license agreement (See http://www.isb-sib.ch/announce/
                                                NINVKAAERQQNIDEQKTALTVNGYAKEAGDKQYRAGLRIEHTRDSEKTTRTENSASSLS
                                                                                    K---DKGENGSSTDEGEGLVT----AKEVIDAVNKAGWRM-----
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1608 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Toxin; Outer membrane; Signal.
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(Rel. 14,
(Rel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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annotation
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Pred. No. 0.12;
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OMPA_RICRI
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01-APR-1990
01-APR-1990
16-OCT-2001
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01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein A precursor (190 kDa a antigen) (rOmpA) (rOmp A).
                                                              CHAIN
DOMAIN
                                                                                                    Antigen;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anderson B.E., McDonald G.A., Jones D.C., Re "A protective protein antigen of Rickettsia repeated, near-identical sequences.";

Infect. Immun. 58:2760-2769(1990).

INFORMATION: ELICITS PROTECTIVE INJUNITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rickettsiaceae;
NCBI_TaxID=783;
                                                                                                                                                                                                                                                                                             modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OMPA_RICRI
LerPro; IFANOUS LEADURE LETPRO 1 PRO05546; Autoliu...., am; PR03797; Autolransporter; 1.
am; PR03797; Autolransporter; 3.
iGRFAMS; TIGR01414; autolrans_barl; 3.
iGRFAMS; TIGR01414; autolrans_barl; 3.
iGRFAMS; TIGR01414; autolrans_barl; 3.
iGRFAMS; TIGR01414; autolrans_barl; 5.
iGRFAMS; TIGR01414; autolrans_barl; 3.
iGRFAMS; TIGR014141; autolrans_barl; 3.
iGRFAMS; TIGR01414; autolrans_barl; 3.
iGRFAMS; TIGR0141414; autolrans_barl; 3.
iGRFAMS; TIGR0141414; autolrans_barl; 3.
iGRFAMS;
                                                                                                                                                                                                                     EMBL; M31227; AAA26380.1; -. PIR; A41477; A41477.
                                                                                                                                                                                                                                                                               or send
                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90354033; PubMed=2117568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Alphaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rickettsia rickettsii.
                                                                                                                                          TIGRFAMS;
                                                                                                                                                                Pfam;
                                                                                                                                                                                InterPro;
                                                                                                                                                                                                InterPro; IPR006315;
                                                                                                                                                                                                                                                                                                                                                                                                                                    - I - SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: CELL WALL. S-LAYER WITH HEXAGONAL SYMMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM: GLYCOSYLATED (PROBABLE).
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16-OCT-2001
                                                                                                                                      ICEN_XANCT P18127;
   NCBI_TaxID=343;
               Xanthomonadaceae;
                                Bacteria; Proteobacteria;
                                            Xanthomonas campestris (pv.
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                                                                                                                                                                                                                                                   EAGYAIGY---SSISDGGNWIIK-------GTASGNSRGH---FGASASVG
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                                Gammaproteobacteria;
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                                               translucens)
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Pred. No. 0.18,
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                                 Xanthomonadales;
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SEQUENCE FRO
STRAIN=X56S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR000258; Ice_nucleatn.
Pfam; PF00818; Ice_nucleation; 81.
PRINTS; PR00327; ICENUCLEATN
PROSITE; PS00314; ICE_NUCLEATION; 57.
Ice nucleation; Repeat; Outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Conserved repetition in the ice nucleation Xanthomonas campestris pv. translucens."; Mol. Gen. Genet. 223:163-166(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X52970; CAA37140.1; -. HSSP; P06620; 1INA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ÷
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91080859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ice nucleation; ReposeDuence 1567 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS OCTAPRETIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF IC SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
                                1166
                                                                                                                                                  1062
                                                                                                                                                                                                          1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: ICE NUCLEATION PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Outer membrane (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRYSTALLIZATION IN SUPERCOOLED WATER.
                                                                                        1114 LIAGYGSTQTAGYD-----
                                                                                                                      371
                                                                                                                                                                               311
                                                                                                                                                                                                                                                                   962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107;
    477
                                                           424
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                                                                                                                                                                                                                                                                                                                                                                                      862
                                                                                                                                                                                                                                                                                                                                                                                                                                               808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                VIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Orser C
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                                                           VDGNARAGIAQAIATA-GLVQAYLPGKSMMAIGGGTYRGEAGY----AIGYSSISDGG--
                                                                                                                      TLSVDGDALNVGSKKDNKPVRITNVAPGV-----
                                                                                                                                                  ADSTLIAGYGSTQTAGSDSSLTAGYGST-QTARQGSDI-----TAGYGSTGT-AGADSS
                                                                                                                                                                             SSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAP
                                                                                                                                                                                                          STGTAGADSTLIAGYGSTQTAGSD--SSLTAGY--
                                                                                                                                                                                                                                      ETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAG
                                                                                                                                                                                                                                                                   GTAGADSTLIAG-----YGSTQTSGS-----DSSLTAGYGSTQTAREGSDVTAGYG
                                                                                                                                                                                                                                                                                                                           -- DV-TAGYGSTGTAGADSTLIAGYGSTQTSGSDSSLTAGYGSTQTARKGSDMTAGYGST
                                                                                                                                                                                                                                                                                                                                                        VKDVLNAGWNIKGVKNVD--FVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTS
                                                                                                                                                                                                                                                                                                                                                                                      YGSTGTAGADSTLISGYG-
                                                                                                                                                                                                                                                                                                                                                                                                                -----SVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDRAAS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                               SDITAGYGSTGTAGADSTLIAGYGSTQTSGSDSSLTAGYG-----STQTAREGSDVTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SELTRNHTKRASATVKTAVLATLLFATVQASANTLKAGDNLKIKQFTYSLKKDLTDLT--
                              YGSTQTAGYNSILTTGYGSTQTAQESSSLTAGYGST--STAGYDSTLTAGYGSTQTAGYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=2259339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152548 MW;
                                                                                                                                                                                                                                                                                                                                                                                     -------STQTAGSDSSLTA---GYGSTQTARKGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 172;
Pred. No. 0.
                                                                                         -SNLTAGYGSTQTAREDSSLTAGYGSTSTAGHDSSLIAG
    FGASASVGYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C8B451D959ECAD63 CRC64;
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                                                                                                                      -KEGDVTNVAQLKGVAQNLNNRIDN
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                                                                                                                                                                                                          -GSTQTARQGSDVTAGYGSTGTAG
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01-AUG-1990 (Rel. 15,
01-NOV-1990 (Rel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Nucleotide sequencing of the Proteus mirabilis calcium-independent hemolysin genes (hpmA and hpmB) reveals sequence similarity with the Serratia marcescens hemolysin genes (shlA and shlB).";
J. Bacteriol. 172:1206-1216(1990).
-I- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P16466;
01-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M30186; AAA25657.1; PIR; A35140; A35140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hemolysin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HLYA_PROMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hemolysis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90170827; PubMed=2407716; Uphoff T.S., Welch R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AN STRAIN-Isolate 477-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Outer membrane.
MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMA
MAY BE RESPONSIBLE FOR PORE FORMATION.
SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REQUIRES HPMB FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: CELL-BOUND HEMOLYSIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CELL MEMBRANES AND CAUSE CELL RUPTURE DEFINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1224
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    197
                                                                                                                                                                                                                                                                                                                 710
                                                                                       159
                                                                                                                                                                                                                                                                                                                                                                                                        129;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           non-profit institutions as long as its content and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                          TRNHTKRASATVKTAVLATLLFATVQASANTLK------AGDNLKIKQFTYSLKKDLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLTSVGTEKLSFSANGNKVNITSD---
                                           KKAIEDGVNTTKPGNNTDLTKKVTARDAIANLANLSNLETPNVGVEVGIKGGGSQQSQTD
                                                                                                                                                                                                                         DTTISG--GFSYTGGVDKVGSKADFQYDKQHTQTEVTKNRGSQTEVAGDLTITANKDLLH
                                                                                                                                                                                                                                                                                                              TSTETEQANSTISGANVDLQANKDVTFAGSDLKTTAGNASITGDNVAFVSTENKKQTDNT 769
                                                                                          EFLSADTKTTTVNVESKDNGKK---
                                                                                                                                   EGASHHVEGRYQESGENIQHL-----AVNDSETSKTDSLNVGIDV-GV-NLDYSGVTKPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toxin; Outer membrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30
1577
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AΑ;
                                                                                                                                                                             ----TNGDTTVHLNGIGSTLTDRAASVKDVLNAGWNIKGVKNVDFVRTYDTV
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21.7%; pre
72;
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 169.5;
Pred. No. 0.18
72; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HEMOLYSIN
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  -DKGENGSSTDEGEGLVTAKEVIDA-VNKAGWRMKTTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rickettsiaceae;
NCBI_TaxID=781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OMPB OR RC1085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9KKA3;
                                                                                                                                                                                                                                                                     Stenos
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Mechanisms
                                                                                                            SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1090
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
(rOmp B) (Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptidel)
                                                                                                                                       "The rickettsial outer membrane protein A and B genes of Richaustralis, the most divergent rickettsia of the spotted fever submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases -i- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ogata H., Audic S., Samson D., Roux V., Raoult D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiffren P.,
Samson D., Roux V., Cossart P., Weissenbac
                                                                                                                                                                                                                                                                                   "Phylogenetic analysis of members of the genus Rickettsia gene coding the outer-membrane protein rOmpB (ompB)."; Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=Malish 7;
                                                                                                                                                                                                                                                                                                                                                     STRAIN=Indian tick typhus, and Mal
MEDLINE=20393643; PubMed=10939649;
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SUBCELLULAR LOCATION: CELL WALL. THIS BACTERI LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY) SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/C
                                                     FUNCTION: THE 32 KDA BETA PEPTIDE MAY (BY SIMILARITY).
                                                                                                        STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE VIRULENCE FACTOR AND/OR IMMUNOGEN DURING
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Q9KK98; Q9XC45;
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EMBL; AF123721; AAF34124.1;
EMBL; AF123726; AAF34129.1;
EMBL; AF149110; AAD39533.1;
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InterPro; IPR005546; Autotransporter.
Pfam; PF03797; Autotransporter; 1.
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120 kDa SURFACE-EXPOSED PROTEIN.

32 kDa BETA PEPTIDE.

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G -> G (IN REF. 3).
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                                              Query Match
Best Local
Matches 15
                                                                                                                                                                                    Antigen;
CHAIN
CHAIN
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rickettsii is encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gilmore R.D. Jr., Joste N., McDonald G.A.; "Cloning, expression and sequence analysis of the gene encoding 120 kD surface-exposed protein of Rickettsia rickettsii."; mol. Microbiol. 3:1579-1586(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Outer membrane protein B (Surface protein antigen) (rOmp B) [Contains: 120 k
                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                            PIR; S18227; S18227.
InterPro; IPR006315; Autotransport.
InterPro; IPR005546; Autotransporter.
Pfam; PF03797; Autotransporter; 1.
TIGRFAMS; TIGR01414; autotrans_barl;
                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 evidence for protein processing from a large precursor."; mol. Microbiol. 5:2361-2370(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antigen) (120 kDa outer membrane protein ompB);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q53047;
30-MAY-2000
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30-MAY-2000 (Rel. 39, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OMPB_RICRI
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NCBI_TaxID=783;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                             Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: THE 120 kDa SURFACE: EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIBULENCE FACTOR AND/OR IMMUNOCEN DUBLING INFECTION.
SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAYER WITH HEXAGONAL
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                                                                      Similarity
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protein B precursor (168 kDa surf
in antigen) (Cell surface antigen
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Pred. No.
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32 kDa BETA PEPTIDE.
POLY-THR.
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STRAIN-Wilmington;
MEDLINE-94040787; PubMed-8224886;
Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;
"Cloning and sequence analysis of the gene e surface layer protein of Rickettsia typhi.";
Gene 133:129-133(1993).
[2]
                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein B precursor (168 kba surface-layer pro-
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (ro-
(rOmp B) (Contains: 120 kba surface-exposed protein (Surface-
antigen) (120 kba outer membrane protein ompB); 32 kba beta p
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NCBI_TaxID=785;
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Rickettsiaceae; Rickettsieae;
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MEDLINE=92104668; PubMed=1729180;

A Hackstadt T., Messer R., Cieplak W., Peacock M.G.;

A Hackstadt T., Messer R., Cieplak W., Peacock M.G.;

Messer R., Cieplak W., Peacock M.G.;

Tividence for proteolytic cleavage of the 120-kilodalton outer membrane protein of rickettsiae: identification of an avirulent function of the fice state of the 120-kilodalton outer membrane protein in processing.";

Infect. Immun. 60:159-165(1992).

C -i- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VITULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.

C -i- FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS A MEMBRANE ANC:

C -i- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY S-LAYER WITH HEXAGONAL SYMMETRY.

C -i- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
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CONFLICT
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STRAIN-Wilmington;
MEDLINE=92114896; PubMed=1370573;
Ching W.M., Carl M., Dasch G.A.;
"Mapping of monoclonal antibody binding sites on CNBr fragments the S-layer protein antigens of Rickettsia typhi and Rickettsia prowazekii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Piam; PF03797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L04661; AAB48987.1; -. PIR; JN0896; JN0896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
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                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                   TAQQAATT-KSAQNVVSKVNAGAAIND-NDLSGVGSIDFTAAPSVLEFNLINPT----T
                                                                                                                                                                                                                                                                                               TVQASANTLKAGDNLKIKQFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFA 105
                                 QVTFEHLVDVGLGGKTNFKTADSKVIITENASFGST
                                                                                          NGGAANAVIGTDNGAGRAAGFIVSVDNGNAATISGQVYAKDIV--
                                                                                                                                                                               LSADTKTTTVNVESKD----
                                                                                                                                                                                                            QEAPLTLGDNAKIVNGANGILNITNGFVKVSDKTFAGIKTINIGDNQGLMFNTTPDAANA
                                                                                                                                                                                                                                     KETAGTNGDTTVHLNGIGSTL--TDRAASVKDVLNAG---WNIKGVKNVDFVRTYDTVEF
                                                                                                                                                  LNLQGGGNTINFNGRDGTGKLVLVSKNGNATEFNVTGSLGGNLKGVIEFDTTAAAGKLIA
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3797; Autotransporter; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGR01414; autotrans_barl;
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1415
657
842
1071
1306
1645
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   VGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPS-
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1353

120 kDa SURFACE-EXPOSED PROTEIN.

1645

32 kDa BETA PEPTIDE.

1429

MEMBRANE ANCHOR (POTENTIAL).

657

H -> N (IN REF. 2).

842

V -> I (IN REF. 2).

1071

G -> A (IN REF. 2).

1306

G -> S (IN REF. 2).
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No. 0.
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01-OCT-1994 (Rel. 3
28-FEB-2003 (Rel. 4
Wall-associated pro
Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Choi S.K., Fuchier N., Dusterhoft A., Ehrlich S.D., Emmerson P.T., Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
                                                                                                                                                                              "Sequencing of a 65 kb region of containing the lic and cel loci, covering the gnt-sacxy region.", Microbiology 142:3113-3123(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus subtilis.
Bacteria; Firmicutes;
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., "Cloning and sequencing of a 29 kb region of the Bacigenome containing the hut and wapA loci."; Microbiology 141:337-343(1995).
                                                                                                                           MEDLINE=98044033;
                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                MEDLINE=97124196; PubMed=8969509; Yoshida K.-I., Shindo K., Sano H.,
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=168 / BGSClA1;
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Q07833;
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Nature 390:249-256(1997)
IN CELL MEMBRANE METABOLISM
           moto K., Yata K.,
H., Danchin A.;
bacterium Bacillus
                                      в.,
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+ FUNCTION: STILL UNKNOWN. NOT INVOLVED IN C MOTILITY, SECRETION OR DIFFERENTIATION. SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. MAY ΒE

DOMAIN: HAS TWO LIGAND-BINDING DOMAINS; THE N-TERMINUS, HAS 101 AA REPEATS WHICH ARE RESPONSIBLE FOR CELL WALL BINDING; C-TERMINUS CONSISTS OF TWO BLOCKS OF RESIDUES WITH A CONSERV INTO THE MEDIUM. CONSERVED

MOTIF REPEATED 31 TIMES.
SIMILARITY: THE REPEATED MOTIF IN THE C-TERMINUS HAS SOME
SIMILARITY TO THE REPEAT IN E.COLI RHS GROUP OF PROTEINS (RHSA-D).

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REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT DOMAIN REPEAT CHAIN PIR; EMBL; EMBL; EMBL; EMBL; REPEAT DOMAIN SubtiList; BG10797; wapA.
InterPro; IPR003305; CBM\_CenC
InterPro; IPR006530; YD. REPEAT REPEAT SIGNAL Pfam; PF02018; CBM\_4\_9; 1. TIGRFAMs; TIGR01643; YD\_repeat\_2x; ; L05634; AAA22883.1; ; D31856; BAA06656.1; ; D32985; BAA06660.1; ; D83026; BAA11683.1; ; Z99124; CAB1959.1; S32920; 1042 1063 1083 1109 11129 11150 11174 11199 11219 11646 Repeat; 29 504 504 636 769 S32920. 28 2334 869 605 736 1040 1061 1082 1102 11102 11128 11148 11169 11193 1218 11238 11238 2139 Signal; Complete proteome.
OR 32 (POTENTIAL).
WALL-ASSOCIATED PROTEIN.
3 X 101 AA APPROXIMATE TA 1-3.
31 X 21 AA APPROXIMATE TANDEM REPEATS OF X(4)-G-X(4)-[YF]-X-D-X(2)-G-X(4).
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2-2.
2-3.
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2-5.
2-6.
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2-11. 17. TANDEM REPEATS

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STANDARD;

PRT; 1025 AA.

935828; Q46015; Q9RFI2;

101-JUN-1994 (Rel. 29, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

58-Fayer protein (Paracrystalline surface layer RSAA OR CC1007)

Caulobacter crescentus.
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REPEAT
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  SEQUENCE FROM N.A.,
                    Caulobacteraceae;
NCBI_TaxID=155892;
                                       Bacteria; Proteobacteria; Alphaproteobacteria;
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                                                                                                                                                                                                  PVRITNVAPGVKEG--DVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIA 437
                                                                                                                                                                                                                                                                 KMKDTEGNVTDIAYD-----
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   EMBL; AF062345; AAC38665.2;
EMBL; AF193063; AAF19365.1;
EMBL; AE005779; AAK22991.1;
PIR; A48995; A48995.
                                                                                                                                                                                                                                                                                                                  MEDLINE=98292737; Pu
Awram P., Smit J.K.;
                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION.
STRAIN-ATCC 19089
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-313
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                                          HSSP; P22629; 1SWC.
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Secreted by an ABC transporter (type I) secretion apparatus.",
J. Bacteriol. 180:3062-3069(1998).

-i. FUNCTION: THE S.-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. PROBABLY ACTS AS
PHYSICAL BARRIER TO PARASITES AND LYTIC ENZYMES.

-i. SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A SELAYER WITH HEXAGONAL SYMMETRY. SECRETED BY AN ABC TRANSPORTER
(TYPE I) SECRETION APPARATUS.

-i. MISCELLANEOUS: THE CALCIUM BINDING OF THIS PROTEIN MAY MEDIATE
SURFACE ATTACHMENT BY IONIC BRIDGING BETWEEN THE S-LAYER AND A
SPECIFIC MEMBRANE-ASSOCIATED OLIGOSACCHARIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-89008089; PubMed-3049545; Fisher J.A., Smit J.K., Agabian N "Transcriptional analysis of the Capital Control of the Capital Control of the Capital Cap
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                                                   the European Bioinformatics Institute. The second by non-profit institutions as long
                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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SEQUENCE FROM N.A.
STRAIN-DSM 3896 / EM1;
MEDLINE-94252998; PubMed-8195085;
Matuschek M., Burchhardt G., Sahm K.,
"Pullulanase of Thermoanaerobacterium
(Clostridium thermosulfurogenes): mole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1994 (Rel. 30, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Amylopullulanase precursor (Alpha-amylase/pullulanase) (Pullulanase type II) [Includes: Alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase); Pullulanase (EC 3.2.1.41) (1,4-alpha-D-glucanohydrolase); 
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P38536;
                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriaceae; Thermoan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Alpha-dextrin endo-1,6-alpha-glucosidase)].
                                                                                                                                                                                                                                                                                                                                                                                                           thermosulfurogenes
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22.9%;
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InterPro; IPR004119; SLH.
Pfam; PP00128; Alpha-amylase_C; 1.
Pfam; PF02806; alpha-amylase_N; 1.
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SMART; SM00060; FN3; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides. CATALYTIC ACTIVITY: Hydrolysis of (1->6)-alpha-D-glucosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO FAMILY 13 OF KNOWN AS THE ALPHA-AMYLASE FAMILY.
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SLH 3.
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28-FEB-2003 (Rel. 41, Last
28-FEB-2003 (Rel. 41, Last
Putative surface-exposed v
BIGA OR STM3478.
Salmonella typhimurium.
                                                                                                                                                                                                                                                   McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Le Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mul Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                  Stojiljkovic I., Valentine P., Heffron F.; "Salmonella typhimurium rhs homolog."; submitted (MAR-1999) to the EMBL/GenBank/DDBJ
                                                                            MEDLINE-91100301; PubMed-1987123; Wu J.Y., Siegel L.M., Kredich N.M.; "High-level expression of Escherichia requirement for a cloned cysG plasmid
                                                                                                                                                                    SEQUENCE OF 1-765
                                                                                                                                                                                                   Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                     STRAIN-LT2 / SGSC1412
MEDLINE-21534948; Publ
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EMBL; A6008859; AAL22340.1; -.
EMBL; M64606; AAA27042.1; ALT_FRAME.
EMBL; M64606; AAA27043.1; ALT_FRAME.
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Peak I.R., Srikhanta Y., Dieckelman M., Moxon R.,
Peak I.R., Srikhanta Y., Dieckelman M., Moxon R.,
Peak I.R., Srikhanta Y., Dieckelman M., Moxon R.,
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D., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.,
genome sequence of Neisseria meningitidis serogroup
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SEQUENCE
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"Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Meningococcus by Whole-Genome (Science 287:1816-1820(2000)). Science 287:4816-1820(2000). EMBL, AF226366; AAR42515.1; -. InterPro; IPRO05594; YadA, 1. Ffam; PF03895; YadA; 1.
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Neisseriaceae; Neisseria.
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Science 287:1816-1820(2000).
EMBL; AF226371; AAAF42520.1; -
InterPro; IPR005594; YadA.
Pfam; PF03885; YadA; 1.
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                                       SKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVG
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        QAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                                       SGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSP
QAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                            SGKGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSP
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ceae; Neisseria.
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RESULT Q9JPS3

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C STRAIN-WGE28;

X MEDLINE-20175756; PubMed=10710308;

REDLINE-20175756; PubMed=10710308;

RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

RA Moxon E.R., Grandi G., Rappuoli R.;

"Identification of Vaccine Candidates Against Serogroup B

"Coming Course By Whole-Genome Sequencing.";
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Q9JPS3;
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01-OCT-2000
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Outer membra
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Neisseria
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                                   AIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
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. 22, Last annotation updat
GNA992.
Betaproteobacteria;
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RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
T'dentification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
REMBL, AF26356, AAF42509.1;
REMBL, AF26356, AAF42509.1;
REMBL, AF263556, AAF42509.1;
REMBL, AF263556, AAF42509.1;
REMBL, AF26357, YadA; 1.
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                                                                  GSSTDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTT
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                                                                                                                                                                 ATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMD
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(TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
ane protein GNA992.
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"Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing."; Science 287:1816-1820(2000).
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"Identification and characterization of a gene
membrane protein of Neisseria meningitidis.";
Submitted (JUN-199) to the EMBL/GenBank/DDBJ d
EMBL; AF126383; AAF42532.1;
EMBL; AF157608; AAK6869.1;
InterPro, IPR005594; Yada.
Pfam; PF03895; Yada; 1.
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Bacteria; Proteobacteria;
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                        KGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASG
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Plizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecch
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., N
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo
Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter
Moxon E.R., Grandi G., Rappuoli R.;
"Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
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81.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Betaproteobacteria;
                                                                                                                                                                                                            2;
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                                                                                                                                                                                                                      Score 2369;
Pred. No. 2
                                                                                                                                                                                                                                                       0881CC094F33B4D4 CRC64;
                                                                                                                                                                                                            Mismatches
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                                                    RAASVKDVLNAGWNIKGVK-----
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                                                                                                                                                                                                                                                                                                                                                                                       Capecchi
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Nuti S.,
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Best Local S
Matches 488
                                                                                                                                                                                                                                                           MEDLINE-20175756; PubMed-10710308;

Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nut Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P. Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H. Hood D.W., Jeffries A.C., Sanders N.J., Granoff D.M., Venter (Moxon E.R., Grandi G., Rappuoli R.;

"Identification of Vaccine Candidates Against Serogroup B"

"Identification of Vaccine Candidates Against Serogroup B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000
01-OCT-2000
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9JPS8;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria
Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Outer membrane
                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                      Meningococcus by Whole-Genome Sequencing Science 287:1816-1820(2000).
                                                                                                                                                                                                                                 InterPro;
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                                 ENTDENTNASSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNG
                                                                          EPVKRTAVVLSERSDKEGTGEKEVTEDSHWGVYFDEKGVLKAGTITLKAGDNLKIKQNTD
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Proteobacteria;
                                                                                                                                                                                                              599
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 22, Last annotation updatane protein GNA992.
                                                                                                                                                                  Conservative
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                                                                                                                                                                                                            62693 MW;
                                           FTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNG
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81.5%;
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Pred.
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No. 2.86
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Zuo P.,
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A Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,

Caleotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.

Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

Baroeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

A Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

Moxon E.R., Grandi G., Rappuoli R.;

"Identification of Vaccine Candidates Against Serogroup B

"Indentification of Vaccine Candidates Against Serogroup B
                                                                                                                                                                                                                 Query Ma
Best Loc
Matches
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01-OCT-2000 (
01-OCT-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=NGE31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                 InterPro; IPR0
Pfam; PF03895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNA992
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488; Conserv
                      65
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ilarity 82.2%;
Conservative
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                      FTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVH
  62114 MW;
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Pred. No. 2.9e
1; Mismatches
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2.9e-96;
nes 13;
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Q93QY4;
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NCBI_TaxID=487;
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Bacteria; Proteobacteria;
Neisseriaceae; Neisseria.
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'fam; PF03895; YadA; 1.
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X MEDLINE-20175755; PubMed-10710308;

A Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

A Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,

A Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

A Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

A Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

A Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

A Moxon E.R., Grandi G., Rappuoli R.;

A Moxon E.R., Grandi G., Rappuoli R.;

Tidentification of Vaccine Candidates Against Serogroup B

"Identification of Vaccine Sequencing.";

Brigger Strain-1816-1820(2000)

L Science 287:1816-1820(2000)

EMBL; AF226369; AAF42525.1;

Brigger Benster Benster Strain Strai
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01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2002 (TrEMBLrel. 2
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                                                                                                                                                                                                                                                                                                          Meningococcus by Whole-Genome Science 287:1816-1820(2000). EMBL; AF226361; AAF42510.1;
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O1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Outer membrane protein GNA992 (NhhA outer membrane GNA992 OR NHHA.
Neisseria meningitidis.
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N. meningitidis PM
A surface protein
N. meningitidis EG
BASBO29 amino acid
A surface protein
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## ALIGNMENTS

RESULT 1 AAY27202 09-OCT-1998; 14-JAN-1998; 01-SEP-1998; WPI; 1999-444400/37. Grandi G, Masignani Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis; bacterial infection; treatment. AAY27202 standard; Protein; 591 14-JAN-1999; WO9936544-A2 Neisseria meningitidis. Amino acid sequence of N. meningitidis protein ORF40-1. 24-SEP-1999 (first entry) (CHIR-) CHIRON SPA. 22-JUL-1999 98GB-0022143. 98GB-0000760. 98GB-0019015. 99WO-IB00103 ۷, Pizza M, Rappuoli R, Scarlato V;

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New protein and its nucleotide sequence, useful in vaccines or diagnostic compositions for treating and/or preventing Neisseria meningitidis infections
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                                  Surface protein;
immunoreactive po
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The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
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DB; AAX85798.
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                 QAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                                                                                    SKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVG
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QAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                               SKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLV
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  The present invention relates to meningitidis mutant polypeptides (AAU06182-AAU06186). The modified
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                                                                                Claim 9; Fig 1;
                                                                                                                  New NhhA surface antigen polypeptides and polynucleotides Neisseria meningitidis, useful in producing vaccines for preventing broad spectrum of Neisseria meningitidis -
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                                                                             Surface protein; immunoreactive p
                                                                                                                 A surface
                                                                                                                                            08-SEP-1999
                                                                                                                                                                                              AAY23741 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ISIS-)
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                                               SKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLV
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New Neisseria NhhA surface antigen polypeptides and polynucleotides sseria meningitidis, useful in producing vaccines for eventing broad spectrum of Neisseria meningitidis treating or S

Claim 9; Fig 1; 91pp; English

The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhha (AAU06182-AAU06185). The modified or mutant Nhha polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectivel immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen Nhha effectively

RESULT 5 AAU06175